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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 11.5 Seconds
(without alignments)
278.878 Million cell updates/sec

Title: US-09-620-586B-12

Perfect score: 630
Sequence: 1 DFGLDCEHSTESRCRCRYPL.....EGQITVGKIPAMVDRCGCS 109

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6C_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	375	3 US-08-891-789B-2	Sequence 2, Appli
2	630	100.0	375	4 US-09-252-149B-2	Sequence 2, Appli
3	630	100.0	375	4 US-09-252-149B-31	Sequence 31, Appli
4	618	98.1	126	2 US-08-525-596B-6	Sequence 6, Appli
5	618	98.1	126	3 US-09-177-860A-6	Sequence 6, Appli
6	618	98.1	126	4 US-09-378-238-6	Sequence 6, Appli
7	618	98.1	126	4 US-09-451-501-6	Sequence 6, Appli
8	618	98.1	130	4 US-09-378-238-21	Sequence 21, Appli
9	618	98.1	225	4 US-09-378-238-19	Sequence 19, Appli
10	618	98.1	375	2 US-08-525-596B-14	Sequence 14, Appli
11	618	98.1	375	2 US-08-765-875-5	Sequence 5, Appli
12	618	98.1	375	3 US-08-795-671-5	Sequence 5, Appli
13	618	98.1	375	3 US-09-177-860A-14	Sequence 14, Appli
14	618	98.1	375	4 US-09-252-149B-29	Sequence 29, Appli
15	618	98.1	375	4 US-09-252-149B-32	Sequence 32, Appli
16	618	98.1	375	4 US-09-252-149B-34	Sequence 34, Appli
17	618	98.1	375	4 US-09-252-149B-35	Sequence 35, Appli
18	618	98.1	375	4 US-09-378-238-14	Sequence 14, Appli
19	618	98.1	375	4 US-09-451-501-14	Sequence 14, Appli
20	618	98.1	375	4 US-09-451-501-19	Sequence 19, Appli
21	618	98.1	375	4 US-09-451-501-21	Sequence 21, Appli
22	618	98.1	375	4 US-09-451-501-23	Sequence 23, Appli
23	618	98.1	375	4 US-09-451-501-27	Sequence 27, Appli
24	618	98.1	376	2 US-08-525-596B-12	Sequence 12, Appli
25	618	98.1	376	3 US-09-177-860A-12	Sequence 12, Appli
26	618	98.1	376	3 US-08-891-789B-6	Sequence 6, Appli
27	618	98.1	376	4 US-09-252-149B-27	Sequence 27, Appli

28	618	98.1	376	4 US-09-252-149B-28	Sequence 28, Appli
29	618	98.1	376	4 US-09-378-238-12	Sequence 12, Appli
30	618	98.1	376	4 US-09-451-501-12	Sequence 12, Appli
31	618	98.1	376	4 US-09-451-501-25	Sequence 25, Appli
32	612	97.1	375	4 US-09-252-149B-30	Sequence 30, Appli
33	608	96.5	375	4 US-09-252-149B-33	Sequence 33, Appli
34	579	91.9	108	2 US-08-525-596B-8	Sequence 8, Appli
35	579	91.9	108	3 US-09-177-860A-8	Sequence 8, Appli
36	579	91.9	108	4 US-09-378-238-8	Sequence 8, Appli
37	579	91.9	108	4 US-09-451-501-8	Sequence 8, Appli
38	573.5	91.0	124	4 US-09-252-149B-24	Sequence 24, Appli
39	573	91.0	126	1 US-08-247-907A-2	Sequence 2, Appli
40	573	91.0	126	1 US-08-452-772-2	Sequence 2, Appli
41	573	91.0	126	2 US-08-765-875-4	Sequence 4, Appli
42	573	91.0	126	3 US-08-795-671-4	Sequence 4, Appli
43	573	91.0	126	4 US-09-414-234-2	Sequence 2, Appli
44	573	91.0	126	4 US-08-919-850-2	Sequence 2, Appli
45	573	91.0	126	5 PCT-US94-05288-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-891-789B-2
; Sequence 2, Application US/08891789B
; Patent No. 6103466
; GENERAL INFORMATION:
; APPLICANT: Grobet, Luc; Georges, Michel
; TITLE OF INVENTION: Double-Muscling in Mammals
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,789B
; FILING DATE: July 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 52836/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-891-789B-2

Query Match 100.0%; Score 630; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYCSGEGHFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYCSGEGHFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKMSPIINMLYFNGEGQITVGKIPAMVDRCGCS 109
DB 327 VHQANPRGSAGPCTPTKMSPIINMLYFNGEGQITVGKIPAMVDRCGCS 375

RESULT 2

US-09-252-149B-2
; Sequence 2, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamed
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: bos taurus
US-09-252-149B-2

Query Match 100.0%; Score 630; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIIAPKRYKANYSGECEFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIIAPKRYKANYSGECEFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375

RESULT 3

US-09-252-149B-31
; Sequence 31, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamed
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 31
; LENGTH: 375
; TYPE: PRT
; ORGANISM: bos taurus
US-09-252-149B-31

Query Match 100.0%; Score 630; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIIAPKRYKANYSGECEFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIIAPKRYKANYSGECEFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375

RESULT 4
US-08-525-596B-6

; Sequence 6, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-525-596B-6

Query Match 98.1%; Score 618; DB 2; Length 126;
Best Local Similarity 98.2%; Pred. No. 4.2e-65;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIIAPKRYKANYSGECEFVFLQKYPHTL 60
DB 18 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIIAPKRYKANYSGECEFVFLQKYPHTL 77
QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 78 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 126

RESULT 5

US-09-177-860A-6
; Sequence 6, Application US/09177860A
; Patent No. 6096506
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-177-860A-6

Query Match 98.1%; Score 618; DB 3; Length 126;
Best Local Similarity 98.2%; Pred. No. 4.2e-65;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 18 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 77

OY 61 VHQANPRGSAGPCTPTKSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 78 VHQANPRGSAGPCTPTKSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 126

RESULT 6

US-09-378-238-6
Sequence 6, Application US/09378238
Patent No. 6465239
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
FILE REFERENCE: JHU1120-9
CURRENT APPLICATION NUMBER: US/09/378,238
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1997-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1994-03-18
EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 126
TYPE: PRT
ORGANISM: Mus musculus
US-09-378-238-6

Query Match 98.1%; Score 618; DB 4; Length 126;
Best Local Similarity 98.2%; Pred. No. 4.2e-65;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60

DB 18 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 77
OY 61 VHQANPRGSAGPCTPTKSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 78 VHQANPRGSAGPCTPTKSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 126

RESULT 7

US-09-451-501-6
Sequence 6, Application US/09451501
Patent No. 6468535
GENERAL INFORMATION:
APPLICANT: Se-Jin Lee et al.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/451,501
FILING DATE: 30-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,071
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US94/03019
FILING DATE: 18-March-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/105001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-451-501-6

Query Match 98.1%; Score 618; DB 4; Length 126;
Best Local Similarity 98.2%; Pred. No. 4.2e-65;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 18 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 77

OY 61 VHQANPRGSAGPCTPTKSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 78 VHQANPRGSAGPCTPTKSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 126

RESULT 8

US-09-378-238-21
Sequence 21, Application US/09378238
Patent No. 6465239
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin


```
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
; TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
; TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
; FILE REFERENCE: JHU1120-9
; CURRENT APPLICATION NUMBER: US/09/378,238
; EARLIER FILING DATE: 1999-08-19
; EARLIER APPLICATION NUMBER: 08/795,071
; EARLIER FILING DATE: 1997-02-05
; EARLIER APPLICATION NUMBER: 08/525,596
; EARLIER FILING DATE: 1995-10-25
; EARLIER APPLICATION NUMBER: PCT/US94/03019
; EARLIER FILING DATE: 1994-03-18
; EARLIER APPLICATION NUMBER: 08/033,923
; EARLIER FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-378-238-21
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Query Match          98.1%; Score 618; DB 4; Length 130;
Best Local Similarity 98.2%; Pred. No. 4.3e-65;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCEFFVLQKYPHTL 60
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Db 22 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCEFFVLQKYPHTL 81
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QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
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Db 82 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 130
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RESULT 9

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US-09-378-238-19
; Sequence 19, Application US/09378238
; Patent No. 6465239
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
; TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
; TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
; FILE REFERENCE: JHU1120-9
; CURRENT APPLICATION NUMBER: US/09/378,238
; EARLIER FILING DATE: 1999-08-19
; EARLIER APPLICATION NUMBER: 08/795,071
; EARLIER FILING DATE: 1997-02-05
; EARLIER APPLICATION NUMBER: 08/525,596
; EARLIER FILING DATE: 1995-10-25
; EARLIER APPLICATION NUMBER: PCT/US94/03019
; EARLIER FILING DATE: 1994-03-18
; EARLIER APPLICATION NUMBER: 08/033,923
; EARLIER FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-378-238-19
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Query Match          98.1%; Score 618; DB 4; Length 225;
Best Local Similarity 98.2%; Pred. No. 8.3e-65;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCEFFVLQKYPHTL 60
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Db 117 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCEFFVLQKYPHTL 176
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QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
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Db 177 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 225
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RESULT 10

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US-08-525-596B-14
; Sequence 14, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
US-08-525-596B-14
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Query Match          98.1%; Score 618; DB 2; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCEFFVLQKYPHTL 60
|||||
Db 267 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCEFFVLQKYPHTL 326
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```
QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
|||||
Db 327 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 375
```

RESULT 11

```
US-08-765-875-5
; Sequence 5, Application US/08765875
; Patent No. 5914234
; GENERAL INFORMATION:
; APPLICANT: LEE, SE-JIN
; APPLICANT: MCPHERSON, ALEXANDRA C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: SPENSLAY HORN JUBAS & LUBITZ
```


STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,875
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/706,958
FILING DATE:
APPLICATION NUMBER: US/08/272,763
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN PH.D., LISA A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD3641
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-8
FEATURE:
NAME/KEY: Protein
LOCATION: 1..375
US-08-765-875-5

Query Match 98.1%; Score 618; DB 2; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHESTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYCSGECEVFLOKYPHTHL 60
DB 267 DFGIDCDHESTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYCSGECEVFLOKYPHTHL 326

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 375

RESULT 12
US-08-795-671-5
Sequence 5, Application US/08795671
Patent No. 6008434
GENERAL INFORMATION:
APPLICANT: Se-jin Lee and Alexandra McPherron
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,671
FILING DATE: February 6, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/106001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-8
FEATURE:
NAME/KEY: Protein
LOCATION: 1..375
US-08-795-671-5

Query Match 98.1%; Score 618; DB 3; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHESTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYCSGECEVFLOKYPHTHL 60
DB 267 DFGIDCDHESTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYCSGECEVFLOKYPHTHL 326

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 375

RESULT 13
US-09-177-860A-14
Sequence 14, Application US/09177860A
Patent No. 6096506
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-177-860A-14

Query Match 98.1%; Score 618; DB 3; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLQKYPHTL 60
DB 267 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 375

RESULT 14

US-09-252-149B-29
; Sequence 29, Application US/09252149B

; Patent No. 6369201

; GENERAL INFORMATION:

; APPLICANT: Barker, Christopher A.

; APPLICANT: Morsey, Mohamad

; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN

; TITLE OF INVENTION: VERTEBRATE SUBJECTS

; FILE REFERENCE: 9001-0042

; CURRENT APPLICATION NUMBER: US/09/252,149B

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: 60/075,213

; PRIOR FILING DATE: 1998-02-19

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 29

; LENGTH: 375

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-252-149B-29

Query Match 98.1%; Score 618; DB 4; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLQKYPHTL 60
DB 267 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 375

RESULT 15

US-09-252-149B-32

; Sequence 32, Application US/09252149B

; Patent No. 6369201

; GENERAL INFORMATION:

; APPLICANT: Barker, Christopher A.

; APPLICANT: Morsey, Mohamad

; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN

; TITLE OF INVENTION: VERTEBRATE SUBJECTS

; FILE REFERENCE: 9001-0042

; CURRENT APPLICATION NUMBER: US/09/252,149B

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: 60/075,213

; PRIOR FILING DATE: 1998-02-19

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 32
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-252-149B-32

Query Match 98.1%; Score 618; DB 4; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLQKYPHTL 60
DB 267 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 375

Search completed: January 31, 2003, 18:18:23
Job time : 11.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 32 Seconds

(without alignments)
453.885 Million cell updates/sec

Title: US-09-620-586B-12

Perfect score: 630
Sequence: 1 DFGLDCEHSTESRCRYPL.....EGQIYKIPAMVDRGCS 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	630	100.0	109	22	AAB20142	Cattle growth diff
2	630	100.0	375	19	AAW69887	Bovine growth diff
3	630	100.0	375	20	AAV33934	Amino acid sequenc
4	630	100.0	375	20	AAV33917	Bovine myostatin s
5	630	100.0	375	20	AAV31191	Bovine GDF-8 prote
6	630	100.0	375	22	AAB20135	Cattle growth diff
7	630	100.0	375	23	AAE18664	Bovine growth diff
8	630	100.0	375	23	AAU75625	Bovine promyostati
9	624	99.0	375	20	AAW97884	Bovine myostatin.
10	618	98.1	109	22	AAB20141	Human growth diffe

11	618	98.1	109	23	AAW51935	Human TGFbeta prot
12	618	98.1	126	15	AAW63161	Mouse growth diffe
13	618	98.1	126	19	AAW69883	Murine growth diff
14	618	98.1	126	20	AAV15386	C-terminal region
15	618	98.1	126	22	AAW73182	Murine GDF-8 #1.
16	618	98.1	130	22	AAW73189	Rat GDF-8. Rattus
17	618	98.1	160	22	AAW20153	Growth differentia
18	618	98.1	226	22	AAW73188	Chicken GDF-8. Ga
19	618	98.1	254	22	AAW20152	Growth differentia
20	618	98.1	362	22	AAW20132	Turkey growth diffe
21	618	98.1	374	23	AAU75623	Chicken promyostat
22	618	98.1	375	15	AAW63160	Human growth diffe
23	618	98.1	375	19	AAW69888	Human growth diffe
24	618	98.1	375	19	AAW69891	Pig growth diffe
25	618	98.1	375	19	AAW69885	Human growth diffe
26	618	98.1	375	19	AAW65460	Human growth diffe
27	618	98.1	375	20	AAV33838	Amino acid sequenc
28	618	98.1	375	20	AAV33839	Amino acid sequenc
29	618	98.1	375	20	AAV33840	Amino acid sequenc
30	618	98.1	375	20	AAV33841	Amino acid sequenc
31	618	98.1	375	20	AAV33843	Amino acid sequenc
32	618	98.1	375	20	AAV33844	Amino acid sequenc
33	618	98.1	375	20	AAV33937	Amino acid sequenc
34	618	98.1	375	20	AAV33938	Amino acid sequenc
35	618	98.1	375	20	AAV33932	Amino acid sequenc
36	618	98.1	375	20	AAV33935	Amino acid sequenc
37	618	98.1	375	20	AAV31189	Human GDF-8 protei
38	618	98.1	375	20	AAV31192	Chicken GDF-8 prot
39	618	98.1	375	20	AAV31194	Turkey GDF-8 prote
40	618	98.1	375	20	AAW97887	Human myostatin.
41	618	98.1	375	21	AAW21087	Human GDF-8. Homo
42	618	98.1	375	21	AAV92035	Human growth diffe
43	618	98.1	375	21	AAV77566	Human growth diffe
44	618	98.1	375	22	AAW73187	Human GDF-8 #2. H
45	618	98.1	375	22	AAW20131	Human growth diffe

ALIGNMENTS

RESULT 1	
AAB20142	
ID	AAB20142 standard; Protein; 109 AA.
XX	
AC	AAB20142;
XX	
DT	30-APR-2001 (first entry)
XX	
DE	Cattle growth differentiation factor 8 C-terminal region.
XX	
KW	Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
KW	vaccine; muscle; meat; cachexia; cardiac; cattle; mutant; mutein.
XX	
OS	Bos taurus.
OS	Synthetic.
XX	
PN	WO200105820-A2.
XX	
PD	25-JAN-2001.
XX	
PF	20-JUL-2000; 2000WO-DK00413.
XX	
PR	20-JUL-1999; 99DK-0001014.
PR	26-JUL-1999; 99US-0145275.
XX	
XX	(MEBI-) M & B BIOTECH AS.
XX	
PI	Halkier T, Mouritsen S, Klyener S;
XX	
DR	WPI; 2001-112680/12.
XX	
PT	Increasing the muscle mass of animals used in meat production by down
PT	regulating growth differentiation factor 8 (GDF-8) activity in the

PT animal through induction of anti-GDF-8 antibody production -
XX
PS Claim 17, Page 94-95; 110pp; English.
XX

CC The present sequence comprises the 109 amino acid residue
CC C-terminal region of cattle growth differentiation factor 8
CC (GDF-8), i.e. residues 267-375 of the full-length protein (see
CC AAB20132). The homodimer of this region is thought to be the
CC biologically active form of GDF-8. It is an object of the
CC invention to produce a recombinant therapeutic vaccine capable of
CC effecting down-regulation of GDF-8 in order to increase the muscle
CC growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)
CC are provided that are capable of breaking autotolerance against
CC autologous GDF-8. These comprise the C-terminal portion of human
CC GDF-8 in which a portion of the native sequence is replaced by a
CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
CC P2 or P30. The high number of Cys residues in the C-terminal region
CC limits the possible sites in which the T-cell epitope can be
CC positioned without major disturbance of the native 3-dimensional
CC structure of the protein. Nucleic acids encoding the GDF-8 variants
CC can be used for genetic immunisation of the animals. Down-regulation
CC of GDF-8 activity can increase muscle mass by up to at least 45% in
CC cattle, pigs and poultry used for meat production, reducing the need
CC for antibiotic feed-additives. Anti-GDF8 vaccines can be used to
CC treat human diseases such as cancer cachexia where muscle atrophy is
CC pronounced and for patients suffering from acute and chronic heart
CC failure.
XX

SQ Sequence 109 AA;

Query Match 100.0%; Score 630; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYSGECEVFLOKYPHTL 60
DB 1 DFGLDCEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYSGECEVFLOKYPHTL 60
QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109

RESULT 2

ID AAW69887 standard; Protein; 375 AA.

AC AAW69887;

DT 07-DEC-1998 (first entry)

DE Bovine growth differentiation factor-8.

KW Growth differentiation factor-8; GDF-8; human; transgenic animal;
KW transforming growth factor-beta; muscle; meat; inhibitor; obesity;
KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
therapy.
XX
OS Bos taurus.

Key Location/Qualifiers
FT Cleavage-site 263..266
FT Protein 267..375
FT /label= Mat_protein

PN WO9833887-A1.

PD 06-AUG-1998.

PF 05-FEB-1998; 98WO-US02479.

PR 23-MAY-1997; 97US-0862445.
PR 05-FEB-1997; 97US-0795071.

PR 28-APR-1997; 97US-0847910.

PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

PI Lee S, McPherron AC;

DR WPI; 1998-437444/37.

DR N-PSDB; AAV45818.

PT Transgenic animals with gene for growth differentiation factor-8
PT disrupted - have increased muscle and reduced cholesterol contents,
PT also use of GDF-8 inhibitors for treating cancer, obesity,
PT neuromuscular disease
XX

PS Example 9; Fig 14b; 125pp; English.

CC This is the amino acid sequence of bovine growth differentiation
CC factor-8 (GDF-8), a novel member of the transforming growth factor-
CC beta superfamily that appears to relate to various cell
CC proliferative disorders, especially those involving muscle, nerve
CC and adipose tissue. The sequence was deduced from a cDNA clone
CC (see AAV45818) isolated from a skeletal muscle cDNA library. The
CC invention provides novel mammalian and avian GDF-8 proteins (see
CC AAW69883-92). A transgenic non-human animal is claimed in which
CC GDF-8 expression is disrupted or interfered with. Also claimed
CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
CC from these animals; (2) method for increasing muscle mass in
CC animals by administering an antibody (Ab) that binds to GDF-8; (3)
CC inhibiting the action of GDF-8 by treating foetal or adult muscle
CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
CC acid encoding a GDF-8 protein truncated by loss of the C-terminal
CC active fragment. The transgenic animals have increased muscle mass
CC and for poultry reduced cholesterol contents. Method (3) is used
CC to treat muscle wasting or neuromuscular diseases, muscular atrophy
CC and aging, particularly muscular dystrophy, spinal cord or
CC traumatic injuries, congestive or obstructive lung disease, AIDS
CC and cachexia. Method (4) is used to treat cancer of muscle,
CC connective tissue and bone, or obesity. Also (not claimed) GDF-8
CC can be used to maintain myoblasts intended for transplanting or to
CC improve efficiency of fusion. Ab can be used to detect and
CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
CC also for immunotherapy and in vivo imaging.
XX

SQ Sequence 375 AA;

Query Match 100.0%; Score 630; DB 19; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.7e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYSGECEVFLOKYPHTL 60

DB 267 DFGLDCEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYSGECEVFLOKYPHTL 326

QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109

DB 327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375

RESULT 3

ID AAY33934 standard; peptide; 375 AA.

AC AAY33934;

DT 09-NOV-1999 (first entry)

DE Amino acid sequence of bovine myostatin.

KW Myostatin; mouse; rabbit; human; baboon; bovine; porcine; ovine; chick;
KW turkey; zebrafish; immune response; vaccine; body weight; muscle mass;
KW mammary gland tissue; lactation; feed uptake; muscle degeneration; GDF11.
XX
OS Bos sp.

```

XX PN WO9942573-A1.
XX PD 26-AUG-1999.
XX PF 19-FEB-1999; 99WO-CA00128.
XX PR 19-FEB-1998; 98US-0075213.
XX PA (BIOS-) BIOSTAR INC.
XX PI Barker CA, Morsey M;
XX DR WPI; 1999-527471/44.
XX PT New myostatin peptide, multimers and immunoconjugates for eliciting
XX PT an immune response in a vertebrate against a myostatin immunogen
XX PS Claim 4; Fig 1A-D; 109pp; English.
XX
CC The invention provides myostatin peptides consisting of 3-100 amino
CC acids, derived from a region of mouse, rabbit, human, baboon, bovine,
CC porcine, ovine, chick, turkey or zebrafish myostatin (see sequences
CC AA33930-939). The myostatin peptides are derived preferably from a
CC region of amino acid residues 1-275, 25-300, 50-325 or 75-350 of the
CC above sequences. The peptides and the nucleic acids encoding the peptides
CC are useful as vaccines for eliciting an immune response in a vertebrate
CC against a myostatin immunogen. They result in increasing body weight,
CC muscle mass, number and size of muscle cells, muscle strength, mammary
CC gland tissue, lactation, appetite or feed uptake, life span of the
CC vertebrate, and cause a reduction in body fat content, useful for muscle
CC wasting conditions. The vaccines are also useful for treating a disorder
CC which comprises degeneration or wasting of muscle in a vertebrate, and
CC useful for modulating GDF11 activity. The present sequence represents
CC a bovine myostatin sequence.
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 630; DB 20; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.7e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGIDCDEHSTESRCRRYPLTVDFEAFGWDWITAPKRYKANYCSGCEFFVLOKYPHTL 60
DB 267 DFGIDCDEHSTESRCRRYPLTVDFEAFGWDWITAPKRYKANYCSGCEFFVLOKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 375

RESULT 4
AA33917
ID AA33917 standard; Protein; 375 AA.
XX
AC AA33917;
XX
DT 09-NOV-1999 (first entry)
XX
DE Bovine myostatin sequence.
XX
KM Myostatin; mouse; rabbit; human; baboon; bovine; porcine; ovine; chick;
KM turkey; zebrafish; immune response; vaccine; body weight; muscle mass;
KM mammary gland tissue; lactation; feed uptake; muscle degeneration;
KM GDF11 activity.
XX
OS Bos sp.
XX
FH Key Location/Qualifiers
FH Cleavage-site 263..266
FT /note="proteolytic cleavage site"
FT 264..375
FT Region
FT /note="myostatin active region"

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XX PN WO9942573-A1.
XX PD 26-AUG-1999.
XX PF 19-FEB-1999; 99WO-CA00128.
XX PR 19-FEB-1998; 98US-0075213.
XX PA (BIOS-) BIOSTAR INC.
XX PI Barker CA, Morsey M;
XX DR WPI; 1999-527471/44.
XX DR N-PSDB; AAX99349.
XX PT New myostatin peptide, multimers and immunoconjugates for eliciting
XX PT an immune response in a vertebrate against a myostatin immunogen
XX PS Disclosure; Fig 16B; 109pp; English.
XX
CC The invention provides myostatin peptides consisting of 3-100 amino
CC acids, derived from a region of mouse, rabbit, human, baboon, bovine,
CC porcine, ovine, chick, turkey or zebrafish myostatin (see sequences
CC AA33930-939). The myostatin peptides are derived preferably from a
CC region of amino acid residues 1-275, 25-300, 50-325 or 75-350 of the
CC above sequences. The peptides and the nucleic acids encoding the peptides
CC are useful as vaccines for eliciting an immune response in a vertebrate
CC against a myostatin immunogen. They result in increasing body weight,
CC muscle mass, number and size of muscle cells, muscle strength, mammary
CC gland tissue, lactation, appetite or feed uptake, life span of the
CC vertebrate, and cause a reduction in body fat content, useful for muscle
CC wasting conditions. The vaccines are also useful for treating a disorder
CC which comprises degeneration or wasting of muscle in a vertebrate, and
CC useful for modulating GDF11 activity. The present sequence represents
CC the amino acid sequence of bovine myostatin.
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 630; DB 20; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.7e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGIDCDEHSTESRCRRYPLTVDFEAFGWDWITAPKRYKANYCSGCEFFVLOKYPHTL 60
DB 267 DFGIDCDEHSTESRCRRYPLTVDFEAFGWDWITAPKRYKANYCSGCEFFVLOKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 375

RESULT 5
AA31191
ID AA31191 standard; Protein; 375 AA.
XX
AC AA31191;
XX
DT 29-OCT-1999 (first entry)
XX
DE Bovine GDF-8 protein.
XX
KM GDF-8; growth differentiation factor receptor; GDF-11; therapy; human;
KM veterinary; medicine; treatment; muscle tissue disease; wasting disease;
KM neuromuscular disorder; muscular atrophy; spinal cord injury; aging; fat;
KM traumatic injury; acquired immune deficiency syndrome; cachexia; bovine;
KM congenital obstructive pulmonary disease; transgenic animal; transgene;
KM food animal; cholesterol; muscle mass; diagnostic.
XX
OS Bos taurus.
XX
PN WO9906559-A1.
XX

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PD 11-FEB-1999.
 XX
 PF 28-JUL-1998; 98WO-US15598.
 XX
 PR 01-AUG-1997; 97US-0054461.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Lee S, McPherron A;
 XX
 DR WPI; 1999-153789/13.
 DR N-PSDB; AA209367.
 XX
 PT Recombinant cells that express growth-differentiation factor
 PT receptors - and related antibodies, nucleic acids, vector,
 PT transformed cells, peptide fragments and transgenic animals, for
 PT treatment and diagnosis of muscle tissue diseases
 XX
 PS Examples; Fig 2b; 89pp; English.
 XX
 CC This invention describes novel recombinant cell lines that express
 CC growth-differentiation factor-8 (GDF-8) receptor polypeptide or GDF-11
 CC receptor polypeptide. The GDF receptors are used to identify specific
 CC (ant)agonists, potentially useful therapeutically in human or veterinary
 CC medicine. Antibodies derived from the products of the invention are used
 CC to treat muscle tissue diseases (particularly wasting diseases,
 CC neuromuscular disorders, muscular atrophy and aging, e.g. spinal cord and
 CC traumatic injury, congenital obstructive pulmonary diseases, acquired
 CC immune deficiency syndrome and cachexia). Transgenic, non-human animals
 CC that express the products of the invention from a transgene present in
 CC germ and somatic cells, specifically where GDF-8 receptor is expressed,
 CC may be food animals and have decreased fat and cholesterol contents and
 CC increased muscle mass. Peptides derived from the products of the
 CC invention and GDF-receptor binding and blocking agents, are reagents and
 CC diagnostic agents for studying muscle wasting diseases and for
 CC development of therapeutic agents. This sequence represents the bovine
 CC GDF-8 protein which is used in the method of the invention.
 XX
 SQ Sequence 375 AA;
 Query Match 100.0%; Score 630; DB 20; Length 375;
 Best Local Similarity 100.0%; Pred. No. 6.7e-59;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 60
 DB 267 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 326
 QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
 DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 375
 RESULT 6
 AAB20135
 ID AAB20135 standard; Protein; 375 AA.
 XX
 AC AAB20135;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Cattle growth differentiation factor 8.
 XX
 KW Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
 KW vaccine; muscle; meat; cachexia; cardiant; cattle.
 XX
 OS Bos taurus.
 XX
 PN WO200105820-A2.
 XX
 PD 25-JAN-2001.
 XX
 PF 20-JUL-2000; 2000WO-DK00413.

XX
 PR 20-JUL-1999; 99DK-0001014.
 PR 26-JUL-1999; 99US-0145275.
 XX
 PA (MEBT-) M & E BIOTECH AS.
 XX
 PI Halkier T, Mouritsen S, Klysner S;
 XX
 DR WPI; 2001-112680/12.
 XX
 PT Increasing the muscle mass of animals used in meat production by down
 PT regulating growth differentiation factor 8 (GDF-8) activity in the
 PT animal through induction of anti-GDF-8 antibody production -
 XX
 PS Example 1; Page 82-83; 110pp; English.
 XX
 CC The present sequence is that of cattle growth differentiation factor
 CC 8 (GDF-8), also called myostatin. It is an object of the invention
 CC to produce a recombinant therapeutic vaccine capable of effecting
 CC down-regulation of GDF-8 in order to increase the muscle growth
 CC rate of farm animals. Variants of GDF-8 (see AAB20145-53) are
 CC provided that are capable of breaking autotolerance against
 CC autologous GDF-8. These comprise a C-terminal portion of human
 CC GDF-8 in which a portion of the native sequence is replaced by a
 CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
 CC P2 or P30. Nucleic acids encoding the GDF-8 variants can be used
 CC for genetic immunisation of the animals. Down-regulation of GDF-8
 CC activity is used to increase muscle mass by up to at least 45%
 CC in cattle, pigs and poultry used for meat production, reducing the
 CC need for antibiotic feed-additives. Anti-GDF8 vaccines can be used
 CC to treat human diseases such as cancer cachexia where muscle atrophy
 CC is pronounced and for patients suffering from acute and chronic
 CC heart failure.
 XX
 SQ Sequence 375 AA;
 Query Match 100.0%; Score 630; DB 22; Length 375;
 Best Local Similarity 100.0%; Pred. No. 6.7e-59;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 60
 DB 267 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 326
 QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
 DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 375
 RESULT 7
 AAE18664
 ID AAE18664 standard; Protein; 375 AA.
 XX
 AC AAE18664;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Bovine promyostatin.
 XX
 KW Bovine; promyostatin; myostatin; therapy; amyotrophic lateral sclerosis;
 KW neurodegenerative disease; GDF-11; muscular dystrophy; type II diabetes;
 KW muscle growth; myostatin prodomain; signal transduction; atherosclerosis;
 KW obesity; cachexia; hypertension; myocardial infarction; neuroprotective;
 KW muscular dystrophy; muscle wasting disorder; neuromuscular disorder;
 KW anorexia; growth differentiation factor; anorectic; immunomodulator;
 KW cardiant; metabolic.
 XX
 OS Bos sp.
 XX
 FH Key
 FT Domain
 FT Location/Qualifiers
 20..262
 /note= "Myostatin prodomain; This region is specifically
 claimed in claim 12 of the specification"

FT Region

267..374
/note= "Mature myostatin; This region is specifically
claimed in claim 17 of the specification"

WO200209641-A2.

07-FEB-2002.

26-JUL-2001; 2001WO-US23510.

27-JUL-2000; 2000US-0628112.

(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

Lee S, Mcpherron AC;

WPI; 2002-179989/23.

N-PSDB; AAD29747.

Novel substantially purified promyostatin polypeptide portion
(myostatin prodomain or mature myostatin peptide), useful as myostatin
signal transduction modulator in muscle cell or adipose tissue, for
treating obesity -

Claim 5; Page 157-158; 175pp; English.

The present invention relates to a purified promyostatin polypeptide portion. A myostatin peptide is useful as a target for treatment of neurodegenerative diseases such as amyotrophic lateral sclerosis or muscular dystrophy. A myostatin prodomain inhibits myostatin signal transduction, while mature myostatin peptide referred as myostatin is useful for inducing myostatin signal transduction by interacting specifically with myostatin receptor expressed on the surface of the cell. Modulating myostatin signal transduction is useful for regulating skeletal muscle mass, where promyostatin portion is a negative regulator or muscle growth. Modulating myostatin signal transduction in a muscle cell or adipose tissue is useful for treating pathological conditions associated with myostatin such as obesity and type II diabetes, cachexia, conditions associated with obesity, e.g. atherosclerosis, hypertension, myocardial infarction, muscle wasting disorders such as muscular dystrophy, neuromuscular disorders, or anorexia. Myostatin prodomain is useful for modulating the growth of muscle or adipose tissue in an organism. Myostatin prodomain is useful for increasing muscle mass or reducing fat content of an organism which is useful as a food source, and myostatin peptide is useful for decreasing the growth of muscle tissue in an organism e.g. an organism detrimental to an environment. Mutant promyostatin which has dominant negative activity with respect to myostatin or growth differentiation factor (GDF)-11 is useful for reducing or inhibiting myostatin signal transduction. The present sequence is bovine promyostatin.

SQ Sequence 375 AA;

Query Match 100.0%; Score 630; DB 23; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.7e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVLOKYPHTL 60

DB 267 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVLOKYPHTL 326

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 375

RESULT 8

ID AAU75625 standard; Protein; 375 AA.

XX AC AAU75625;

DT 21-MAY-2002 (first entry)

XX DE Bovine promyostatin.

Bovine; promyostatin; immunomodulator; antidepressant; anorectic;
neuroprotective; antidiabetic; growth differentiation factor receptor;
myostatin receptor; GDF; muscle tissue; adipose tissue; cachexia;
wasting disorder; anorexia; muscular dystrophy; neuromuscular disease;
metabolic disorder; obesity; type II diabetes.

Bos sp.

WO200210214-A2.

07-FEB-2002.

26-JUL-2001; 2001WO-US23615.

27-JUL-2000; 2000US-0626896.

(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

Lee S, Mcpherron AC;

WPI; 2002-217116/27.

N-PSDB; ABK15398.

New growth differentiation factor (GDF) receptors and modulators,
useful for ameliorating wasting disorders such as cachexia, muscular
dystrophy or neuromuscular disease or a metabolic disorder such as
obesity or type II diabetes -

Claim 22; Fig 1; 184pp; English.

The invention relates to a substantially purified growth differentiation factor (GDF) receptor, specifically a myostatin receptor, or its functional peptide portion. Also described is a method of modulating an effect of myostatin on a cell by contacting the cell with an agent that affects myostatin signal transduction in the cell. The method and the receptor are useful for ameliorating the severity of a pathological condition characterised by an abnormal amount, development or metabolic activity of muscle or adipose tissue in a subject, particularly a wasting disorder (e.g. cachexia, anorexia, muscular dystrophy or neuromuscular disease) or a metabolic disorder (e.g. obesity or type II diabetes). The present sequence represents the amino acid sequence of bovine promyostatin.

SQ Sequence 375 AA;

Query Match 100.0%; Score 630; DB 23; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.7e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVLOKYPHTL 60

DB 267 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVLOKYPHTL 326

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 375

RESULT 9

ID AAW97884 standard; Protein; 375 AA.

XX AC AAW97884;

DT 07-JUN-1999 (first entry)

XX DE Bovine myostatin.

Myostatin; cattle; bovine; transforming growth factor beta;
double muscling; muscle hyperplasia; transgenic animal.

XX OS Bos taurus.
XX KW WO9902667-A1.
XX PN 21-JAN-1999.
XX PD 14-JUL-1998; 98WO-IB01197.
XX PF 15-JAN-1998; 98US-0007761.
XX PR 14-JUL-1997; 97US-0891789.
XX PA (UYLI-) UNIV LIEGE.
XX PI Georges M, Grobet L, Ponclet D;
XX DR WPI; 1999-120869/10.
XX DR N-PSDB; AAX24415, AAX24464.
XX PT Increasing muscle mass in mammals - by decreasing myostatin
XX expression
XX PS Claim 19; Page 55; 75pp; English.
XX CC This is the amino acid sequence of bovine myostatin, a member of
XX CC the transforming growth factor beta superfamily, as encoded by the
XX CC wild-type gene (see AAX24415). A mutation of this gene (see AAX24416)
XX CC has been detected in cattle. Cattle of the Belgian Blue breed
XX CC homozygous for the mutant gene are double-muscled. A new method of
XX CC increasing muscle mass of a mammal having myostatin-expressing
XX CC muscle cells, comprises administration of a nucleic acid molecule
XX CC substantially complementary to at least a portion of mRNA
XX CC encoding myostatin and of sufficient length to reduce myostatin
XX CC expression and thus increase muscle mass. A ribozyme may also be
XX CC used. Also claimed are: a method for determining muscular
XX CC hyperplasia (MH) in a mammal using primers based upstream and
XX CC downstream of the mutation; a diagnostic kit for determining
XX CC the genotype of a sample of genetic material; a method for
XX CC determining MH in a mammal; a method for determining double
XX CC muscling in a bovine animal; a method for determining the myostatin
XX CC genotype of an animal; purified myostatin; isolated nucleic acids;
XX CC a microbial host cell; a probe based on the myostatin gene
XX CC mutation; transgenic mammals having MH phenotype; a myostatin
XX CC knockout animal; and a transgenic bovine having a gene encoding
XX CC active myostatin, and a heterologous nucleotide sequence antisense
XX CC to that gene, and optionally further containing a gene encoding a
XX CC nucleic acid sequence with ribozyme activity in transcriptional
XX CC association with the antisense sequence.
SQ Sequence 375 AA;
Query Match 99.0%; Score 624; DB 20; Length 375;
Best Local Similarity 99.1%; Pred. No. 2.9e-58;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 267 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNNGEQIYIGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNNGEQIYIGKIPAMVVDRCGCS 375
RESULT 10
ID AAB20141 standard; Protein; 109 AA.
XX AAB20141;
AC AAB20141;
XX 30-APR-2001 (first entry)
DT Human growth differentiation factor 8 C-terminal region.
XX

XX KW Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
XX KW vaccine; muscle; meat; cachexia; cardiant; human; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200105820-A2.
XX PD 25-JAN-2001.
XX PF 20-JUL-2000; 2000WO-DK00413.
XX PR 20-JUL-1999; 99DK-0001014.
XX PR 26-JUL-1999; 99US-0145275.
XX PA (MEBI-) M & E BIOTECH AS.
XX PI Halkier T, Mouritsen S, Klysner S;
XX DR WPI; 2001-112680/12.
XX PT Increasing the muscle mass of animals used in meat production by down
XX PT regulating growth differentiation factor 8 (GDF-8) activity in the
XX PT animal through induction of anti-GDF-8 antibody production -
XX PS Claim 17; Page 93-94; 110pp; English.
XX CC The present sequence comprises the 109 amino acid residue
XX CC C-terminal region of human growth differentiation factor 8
XX CC (GDF-8), i.e. residues 267-375 of the full-length protein (see
XX CC AAB20131). The homodimer of this region is thought to be the
XX CC biologically active form of GDF-8. It is an object of the
XX CC invention to produce a recombinant therapeutic vaccine capable of
XX CC effecting down-regulation of GDF-8 in order to increase the muscle
XX CC growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)
XX CC are provided that are capable of breaking autotolerance against
XX CC autologous GDF-8. These comprise the C-terminal portion of human
XX CC GDF-8 in which a portion of the native sequence is replaced by a
XX CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
XX CC P2 or P30. The high number (9) of Cys residues in the C-terminal
XX CC region limits the possible sites in which the T-cell epitope can be
XX CC positioned without major disturbance of the native 3-dimensional
XX CC structure of the protein. Nucleic acids encoding the GDF-8 variants
XX CC can be used for genetic immunisation of the animals. Down-regulation
XX CC of GDF-8 activity can increase muscle mass by up to at least 45% in
XX CC cattle, pigs and poultry used for meat production, reducing the need
XX CC for antibiotic feed-additives. Anti-GDF8 vaccines can be used to
XX CC treat human diseases such as cancer cachexia where muscle atrophy is
XX CC pronounced and for patients suffering from acute and chronic heart
XX CC failure.
SQ Sequence 109 AA;
Query Match 98.1%; Score 618; DB 22; Length 109;
Best Local Similarity 98.2%; Pred. No. 3.4e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 1 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNNGEQIYIGKIPAMVVDRCGCS 109
DB 61 VHQANPRGSAGPCTPTKMSPINMLYFNNGEQIYIGKIPAMVVDRCGCS 109
RESULT 11
ID AAM51935 standard; Protein; 109 AA.
XX AAM51935;
AC AAM51935;
XX

DT 01-FEB-2002 (first entry)
XX
DE Human TGFbeta protein superfamily protein GDF8.
XX
KW Human; TGFbeta; transforming growth factor beta; mutant; antagonist;
KW agonist; ectopic bone formation; psoriasis; muscular atrophy; scar;
KW formation; fibrosis; cirrhosis; osteopathic; antipsoriatic;
KW antifibrotic; hepatotrophic; vulnary; GDF8.
XX
OS Homo sapiens.
XX
PN DE10026713-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2000; 2000DE-1026713.
XX
PR 30-MAY-2000; 2000DE-1026713.
XX
PA (SEBA/) SEBALD W.
XX
PI SebalD W, Nickel J;
XX
DR WPI; 2002-042559/06.
XX
PT New mutcin of transforming growth factor-beta superfamily protein,
PT useful for treating or preventing e.g. ectopic bone formation, competes
PT for receptor binding
XX
PS Disclosure; Fig 6; 54pp; German.
XX
CC The present invention relates to mutcins of a chain of a protein which,
CC when in the form of a homodimer, has antagonistic or partial agonistic
CC activity, and where the mutation results in the protein binding with low
CC affinity to its receptor. The protein is a member of the transforming
CC growth factor beta (TGFbeta) superfamily. The mutant sequences of the
CC invention can be used in the treatment of diseases associated with the
CC overexpression of TGFbeta family proteins, including ectopic bone
CC formation, psoriasis, muscular atrophy, scar formation, fibrosis and
CC cirrhosis. The present sequence is the human GDF8 protein.
XX
SQ Sequence 109 AA;

Query Match 98.1%; Score 618; DB 23; Length 109;
Best Local Similarity 98.2%; Pred. No. 3.4e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYSGECEFVFLQKYPHTL 60
DB 1 DFGIDCDHEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYSGECEFVFLQKYPHTL 60

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109

RESULT 12
AAR63161
ID AAR63161 standard; Protein; 126 AA.
XX
AC AAR63161;
XX
DT 23-JUN-1995 (first entry)
XX
DE Mouse growth differentiation factor-8 partial sequence.
XX
KW Growth differentiation factor-8; GDF-8; cell proliferation;
KW adipocyte; obesity; transforming growth factor-beta.
XX
OS Mus musculus.
XX
PN WO9421681-A.
XX

PD 29-SEP-1994.
XX
PF 18-MAR-1994; 94WO-US03019.
XX
PR 19-MAR-1993; 93US-0033923.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
XX
PI Lee S, Mcpherron AC;
XX
DR WPI; 1994-316943/39.
DR Q-PSDB; Q76380.
XX
PT New growth differentiation factor 8 - useful for treatment and
PT diagnosis of cell proliferative disorders esp. of muscle.
XX
PS Disclosure; Page 41; 84pp; English.
XX
CC GDF-8 can be used to maintain cells before transplantation; to
CC improve efficiency of cell fusion and to treat obesity or diseases
CC related to abnormal adipocyte proliferation.
XX
SQ Sequence 126 AA;

Query Match 98.1%; Score 618; DB 15; Length 126;
Best Local Similarity 98.2%; Pred. No. 4e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYSGECEFVFLQKYPHTL 60
DB 18 DFGIDCDHEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYSGECEFVFLQKYPHTL 77

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 78 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 126

RESULT 13
AAW69883
ID AAW69883 standard; Protein; 126 AA.
XX
AC AAW69883;
XX
DT 07-DEC-1998 (first entry)
XX
DE Murine growth differentiation factor-8 C-terminal fragment.
XX
KW Growth differentiation factor-8; GDF-8; mouse; transgenic animal;
KW transforming growth factor-beta; muscle; meat; inhibitor; obesity;
KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
KW therapy.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FH Cleavage-site 13..14
FH Cleavage-site 16..17
FH Protein 17..126
FT /note="mature polypeptide"
XX
PN WO9833887-A1.
XX
PD 06-AUG-1998.
XX
PF 05-FEB-1998; 98WO-US02479.
XX
PR 23-MAY-1997; 97US-0862445.
PR 05-FEB-1997; 97US-0795071.
PR 28-APR-1997; 97US-0847910.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Lee S, Mcpherron AC;

XX WPI; 1998-437444/37.
 DR N-PSDB; AAV45809.
 DR XX Transgenic animals with gene for growth differentiation factor-8
 PT disrupted - have increased muscle and reduced cholesterol contents,
 PT also use of GDF-8 inhibitors for treating cancer, obesity,
 PT neuromuscular disease
 XX
 PS Example 2; Page 58; 125pp; English.
 CC This is the amino acid sequence of the C-terminal portion of mouse
 CC growth differentiation factor-8 (GDF-8), a novel member of the
 CC transforming growth factor-beta superfamily that appears to relate
 CC to various cell proliferative disorders, especially those involving
 CC muscle, nerve and adipose tissue. The sequence was deduced from a
 CC partial genomic clone (see AAV45809). A full-length sequence (see
 CC AAV30689) has been deduced from a cDNA clone (see AAV42113). The
 CC invention provides novel mammalian and avian GDF-8 proteins (see
 CC AAV69883-92). A transgenic non-human animal is claimed in which
 CC GDF-8 expression is disrupted or interfered with. Also claimed
 CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
 CC from these animals; (2) method for increasing muscle mass in
 CC animals by administering an antibody (Ab) that binds to GDF-8; (3)
 CC inhibiting the action of GDF-8 by treating foetal or adult muscle
 CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
 CC acid encoding a GDF-8 protein truncated by loss of the C-terminal
 CC active fragment. The transgenic animals have increased muscle mass
 CC and for poultry reduced cholesterol contents. Method (3) is used
 CC to treat muscle wasting or neuromuscular diseases, muscular atrophy
 CC and aging, particularly muscular dystrophy, spinal cord or
 CC traumatic injuries, congestive or obstructive lung disease, AIDS
 CC and cachexia. Method (4) is used to treat cancer of muscle,
 CC connective tissue and bone, or obesity. Also (not claimed) GDF-8
 CC can be used to maintain myoblasts intended for transplanting or to
 CC improve efficiency of fusion. Ab can be used to detect and
 CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
 CC also for immunotherapy and in vivo imaging.
 CC
 SQ Sequence 126 AA;
 Query Match 98.1%; Score 618; DB 19; Length 126;
 Best Local Similarity 98.2%; Pred. No. 4e-58;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
 DB 18 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 77
 QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGSGQIYIGKIPAMVVDRCGCS 109
 DB 78 VHQANPRGSAGPCCPTPTKMSPINMLYFNGSGQIYIGKIPAMVVDRCGCS 126
 RESULT 14
 AAY15386
 ID AAY15386 standard; Protein; 126 AA.
 AC AAY15386;
 XX
 DT 08-DEC-1999 (first entry)
 DE C-terminal region of mouse Growth Differentiation Factor-8 (GDF-8).
 XX
 KW growth differentiation factor; tissue growth; muscle growth;
 KW cell differentiation; animal feed; muscle disorder;
 KW bone degeneration; nerve degeneration; GDF-8; development;
 KW transforming growth factor beta; TGF-beta.
 XX
 OS Mus musculue.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 13..14

FT /label= Potential_proteolytic_cleavage_site
 FT 16..17
 FT /label= Potential_proteolytic_cleavage_site
 FT /note= "cleavage generates mature protein"
 XX
 PN WO940181-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 05-FEB-1999; 99WO-US02511.
 XX
 PR 28-JUL-1998; 98US-0124180.
 PR 05-FEB-1998; 98US-0019070.
 XX
 PA (UYUO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PI Lee S, McPherron AC;
 XX
 DR WPI; 1999-494289/41.
 DR N-PSDB; AAZ06446.
 XX
 PT New differentiation factor useful for treating neurodegenerative
 PT diseases
 PS Example 2; Fig 2a; 138pp; English.
 CC This is the amino acid sequence of the C-terminal region of the GDF-8
 CC precursor protein. The predicted GDF-8 sequence contains two potential
 CC proteolytic processing sites.
 CC Cleavage of the precursor at the second of these sites would generate
 CC a mature C terminal fragment 109 amino acids in length with a predicted
 CC molecular weight of 12,400.
 CC GDF-8 has been shown to result in increased bone and muscle mass (such
 CC as ribs) when expressed in reduced amounts. GDF-8 minus transgenic
 CC animals and forms of animal feed that can inhibit/reduce production of
 CC GDF-8 are of commercial interest.
 CC GDF-8 expression may also have a role in the therapy of abnormal growth
 CC of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8
 CC antisense molecule or dominant negative polypeptide could be used with
 CC foetal or adult muscle cells, bone cells or progenitor cells. These
 CC agents can be administered to a patient suffering from a disorder such
 CC as muscle wasting disease, neuro muscular disorder, muscle atrophy,
 CC osteoporosis, bone degenerative diseases, obesity or other adipocyte
 CC cell disorders, and aging for example.
 CC
 SQ Sequence 126 AA;
 Query Match 98.1%; Score 618; DB 20; Length 126;
 Best Local Similarity 98.2%; Pred. No. 4e-58;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
 DB 18 DFGLCDDEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 77
 QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGSGQIYIGKIPAMVVDRCGCS 109
 DB 78 VHQANPRGSAGPCCPTPTKMSPINMLYFNGSGQIYIGKIPAMVVDRCGCS 126
 RESULT 15
 AAB73182
 ID AAB73182 standard; Protein; 126 AA.
 AC AAB73182;
 XX
 DT 11-MAY-2001 (first entry)
 DE Murine GDF-8 #1.
 XX
 KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
 KW muscular dystrophy; musculodegenerative disease; tissue repair;

KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease.

OS Mus sp.

PN WO200112777-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22884.

XX 19-AUG-1999; 99US-0378238.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

PI Lee S, McPherron AC;

XX WPI; 2001-211209/21.

DR N-PSDB; AAF63547.

XX New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia -

PS Example 2; Fig 2; 124pp; English.

XX The present invention relates to growth differentiation factor-8 (GDF-8)
CC coding sequences and proteins. The present sequence is a GDF-8 protein,
CC which was isolated in the present invention. GDF-8 is useful for treating
CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
CC muscular dystrophy), musclogenenerative diseases or in tissue repair due
CC to trauma, obesity and disorders related to abnormal proliferation of
CC adipocytes. GDF-8 is also useful for treating malignancies of the various
CC organ systems, particularly cells in muscle or adipose tissues and in
CC gene therapy for the treatment of cell proliferative or immunological
CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
CC treating muscle wasting disease, neuromuscular disorder, spinal cord
CC injury, traumatic injury, congestive obstructive pulmonary disease
CC (COPD), AIDS or cachexia.

XX Sequence 126 AA;

Query Match 98.1%; Score 618; DB 22; Length 126;
Best Local Similarity 98.2%; Pred. No. 4e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEVFLOKYPHTL 60
DB 18 DFGIDCDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEVFLOKYPHTL 77

QY 61 VHQANPRGSAGPCCCTPTKMSPINMLYFNGEQIYGIKIPAMVVDRCGS 109
DB 78 VHQANPRGSAGPCCCTPTKMSPINMLYFNGEQIYGIKIPAMVVDRCGS 126

Search completed: January 31, 2003, 18:20:11
Job time : 33 secs

1
2
3
4
5

6

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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:20:18 ; Search time 8 Seconds

(without alignments)
274.933 Million cell updates/sec

Title: US-09-620-586B-12

Sequence: 630
1 DFGLDCEHSTESRCRCRYPL.....EQGIYKIPAMVVDRCGCS 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:*\n2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep:*\n3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*\n4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*\n5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*\n6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*\n7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep:*\n8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep:*\n9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep:*\n10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*\n11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*\n12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*\n13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*\n14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630	100.0	375	US-09-841-730-12	Sequence 12, Appl
2	630	100.0	375	US-09-859-211-21	Sequence 21, Appl
3	618	98.1	126	US-09-859-211-6	Sequence 6, Appl
4	618	98.1	130	US-09-859-211-33	Sequence 33, Appl
5	618	98.1	226	US-09-859-211-35	Sequence 35, Appl
6	618	98.1	374	US-09-841-730-8	Sequence 8, Appl
7	618	98.1	375	US-09-841-730-2	Sequence 2, Appl
8	618	98.1	375	US-09-841-730-14	Sequence 14, Appl
9	618	98.1	375	US-09-859-211-14	Sequence 18, Appl
10	618	98.1	375	US-09-859-211-23	Sequence 23, Appl
11	618	98.1	375	US-09-859-211-27	Sequence 27, Appl
12	618	98.1	375	US-09-859-211-29	Sequence 29, Appl
13	618	98.1	375	US-09-454-540-5	Sequence 5, Appl
14	618	98.1	376	US-09-841-730-4	Sequence 4, Appl
15	618	98.1	376	US-09-841-730-6	Sequence 6, Appl
16	618	98.1	376	US-09-859-211-12	Sequence 12, Appl
17	618	98.1	376	US-09-859-211-25	Sequence 25, Appl
18	618	98.1	376	US-09-813-398-38	Sequence 38, Appl
19	618	98.1	376	US-09-813-398-38	Sequence 38, Appl

20	618	98.1	376	10	US-09-859-894A-11	Sequence 11, Appl
21	613	97.3	375	10	US-09-859-894A-5	Sequence 5, Appl
22	612	97.1	375	9	US-09-841-730-10	Sequence 10, Appl
23	612	97.1	375	9	US-09-859-211-19	Sequence 19, Appl
24	611	97.0	109	10	US-09-754-826-2	Sequence 2, Appl
25	608	96.5	375	9	US-09-841-730-16	Sequence 16, Appl
26	608	96.5	375	9	US-09-859-211-31	Sequence 31, Appl
27	579	91.9	108	9	US-09-859-211-8	Sequence 8, Appl
28	573	91.0	126	10	US-09-454-540-4	Sequence 4, Appl
29	573	91.0	126	10	US-09-859-894A-4	Sequence 4, Appl
30	573	91.0	407	9	US-09-841-730-25	Sequence 25, Appl
31	573	91.0	407	10	US-09-454-540-2	Sequence 2, Appl
32	573	91.0	407	10	US-09-454-540-6	Sequence 6, Appl
33	573	91.0	407	10	US-09-859-894A-2	Sequence 2, Appl
34	573	91.0	408	9	US-09-813-398-33	Sequence 33, Appl
35	559	88.7	374	9	US-09-841-730-20	Sequence 20, Appl
36	553	87.8	136	9	US-09-841-730-29	Sequence 29, Appl
37	553	87.8	157	9	US-09-841-730-27	Sequence 27, Appl
38	504.5	80.1	128	10	US-09-205-658-317	Sequence 317, App
39	245	38.9	120	10	US-09-813-459-20	Sequence 20, Appl
40	245	38.9	120	12	US-10-115-406-20	Sequence 20, Appl
41	245	38.9	121	9	US-09-859-211-46	Sequence 46, Appl
42	245	38.9	121	9	US-09-880-708-24	Sequence 24, Appl
43	245	38.9	408	9	US-09-813-398-20	Sequence 20, Appl
44	245	38.9	408	9	US-09-813-398-22	Sequence 22, Appl
45	232.5	36.9	118	12	US-10-115-406-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-841-730-12
; Sequence 12, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/09/841, 730
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626, 896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485, 046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054, 461
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Bovine
US-09-841-730-12

Query Match 100.0%; Score 630; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 7.2e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRCRYPLTVDFEAFGWDIIAPRYKANYSGECEFVLOKYPHTL 60
Db 267 DFGDCEHSTESRCRCRYPLTVDFEAFGWDIIAPRYKANYSGECEFVLOKYPHTL 326
QY 61 VHQANPRGSAGCCTPTKXSPINMLYFNGEGQIYKIPAMVVDRCGCS 109
Db 327 VHQANPRGSAGCCTPTKXSPINMLYFNGEGQIYKIPAMVVDRCGCS 375
RESULT 2

```
US-09-859-211-21
; Sequence 21, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 21
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Bovine
US-09-859-211-21

Query Match          100.0%; Score 630; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 7.2e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 267 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTKMSPIINMLYFNGEGQIIYKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTKMSPIINMLYFNGEGQIIYKIPAMVVDRCGCS 375

RESULT 3
US-09-859-211-6
; Sequence 6, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 6
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LENGTH: 126
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-859-211-6

Query Match          98.1%; Score 618; DB 9; Length 126;
Best Local Similarity 98.2%; Pred. No. 4.2e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 18 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 77

QY 61 VHOANPRGSAGPCCPTKMSPIINMLYFNGEGQIIYKIPAMVVDRCGCS 109
DB 78 VHOANPRGSAGPCCPTKMSPIINMLYFNGEGQIIYKIPAMVVDRCGCS 126

RESULT 4
US-09-859-211-33
; Sequence 33, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 33
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-859-211-33

Query Match          98.1%; Score 618; DB 9; Length 130;
Best Local Similarity 98.2%; Pred. No. 4.4e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 22 DFGLDDEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 81

QY 61 VHOANPRGSAGPCCPTKMSPIINMLYFNGEGQIIYKIPAMVVDRCGCS 109
DB 82 VHOANPRGSAGPCCPTKMSPIINMLYFNGEGQIIYKIPAMVVDRCGCS 130

RESULT 5
US-09-859-211-35
; Sequence 35, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
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CURRENT APPLICATION NUMBER: US/09/859,211
: CURRENT FILING DATE: 2001-05-15
: PRIOR APPLICATION NUMBER: 09/019,070
: PRIOR FILING DATE: 1998-02-05
: PRIOR APPLICATION NUMBER: 08/862,445
: PRIOR FILING DATE: 1997-05-23
: PRIOR APPLICATION NUMBER: 08/847,910
: PRIOR FILING DATE: 1997-04-28
: PRIOR APPLICATION NUMBER: 08/795,071
: PRIOR FILING DATE: 1997-02-05
: PRIOR APPLICATION NUMBER: 08/525,596
: PRIOR FILING DATE: 1995-10-26
: PRIOR APPLICATION NUMBER: PCT/US94/03019
: PRIOR FILING DATE: 1994-03-18
: PRIOR APPLICATION NUMBER: 08/033,923
: PRIOR FILING DATE: 1993-03-19
: NUMBER OF SEQ ID NOS: 51
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 35
: LENGTH: 226
: TYPE: PRT
: ORGANISM: Gallus gallus
US-09-859-211-35

Query Match 98.1%; Score 618; DB 9; Length 226;
Best Local Similarity 98.2%; Pred. No. 7.8e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVLOKYPHTL 60
Db 118 DFGDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVLOKYPHTL 177

OY 61 VHOANPRGSAGPCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 109
Db 178 VHOANPRGSAGPCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 226

RESULT 6
US-09-841-730-8
: Sequence 8, Application US/09841730
: Patent No. US20020157126A1
: GENERAL INFORMATION:
: APPLICANT: Lee, Se-Jin
: APPLICANT: McPherron, Alexandra C.
: TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
: TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
: FILE REFERENCE: JH01470-2
: CURRENT APPLICATION NUMBER: US/09/841,730
: CURRENT FILING DATE: 2001-04-24
: PRIOR APPLICATION NUMBER: 09/626,896
: PRIOR FILING DATE: 2000-07-27
: PRIOR APPLICATION NUMBER: 09/485,046
: PRIOR FILING DATE: 2000-01-31
: PRIOR APPLICATION NUMBER: PCT/US98/15598
: PRIOR FILING DATE: 1998-07-28
: PRIOR APPLICATION NUMBER: 60/054,461
: PRIOR FILING DATE: 1997-08-01
: NUMBER OF SEQ ID NOS: 29
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 374
: TYPE: PRT
: ORGANISM: Gallus gallus
US-09-841-730-8

Query Match 98.1%; Score 618; DB 9; Length 374;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVLOKYPHTL 60
Db 266 DFGDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVLOKYPHTL 325

OY 61 VHOANPRGSAGPCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 109
Db 326 VHOANPRGSAGPCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 374

RESULT 7
US-09-841-730-2
: Sequence 2, Application US/09841730
: Patent No. US20020157126A1
: GENERAL INFORMATION:
: APPLICANT: Lee, Se-Jin
: APPLICANT: McPherron, Alexandra C.
: TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
: TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
: FILE REFERENCE: JH01470-2
: CURRENT APPLICATION NUMBER: US/09/841,730
: CURRENT FILING DATE: 2001-04-24
: PRIOR APPLICATION NUMBER: 09/626,896
: PRIOR FILING DATE: 2000-07-27
: PRIOR APPLICATION NUMBER: 09/485,046
: PRIOR FILING DATE: 2000-01-31
: PRIOR APPLICATION NUMBER: PCT/US98/15598
: PRIOR FILING DATE: 1998-07-28
: PRIOR APPLICATION NUMBER: 60/054,461
: PRIOR FILING DATE: 1997-08-01
: NUMBER OF SEQ ID NOS: 29
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 375
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-841-730-2

Query Match 98.1%; Score 618; DB 9; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVLOKYPHTL 60
Db 267 DFGDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVLOKYPHTL 326

OY 61 VHOANPRGSAGPCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 109
Db 327 VHOANPRGSAGPCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 375

RESULT 8
US-09-841-730-14
: Sequence 14, Application US/09841730
: Patent No. US20020157126A1
: GENERAL INFORMATION:
: APPLICANT: Lee, Se-Jin
: APPLICANT: McPherron, Alexandra C.
: TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
: TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
: FILE REFERENCE: JH01470-2
: CURRENT APPLICATION NUMBER: US/09/841,730
: CURRENT FILING DATE: 2001-04-24
: PRIOR APPLICATION NUMBER: 09/626,896
: PRIOR FILING DATE: 2000-07-27
: PRIOR APPLICATION NUMBER: 09/485,046
: PRIOR FILING DATE: 2000-01-31
: PRIOR APPLICATION NUMBER: PCT/US98/15598
: PRIOR FILING DATE: 1998-07-28
: PRIOR APPLICATION NUMBER: 60/054,461
: PRIOR FILING DATE: 1997-08-01
: NUMBER OF SEQ ID NOS: 29
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14
: LENGTH: 375
: TYPE: PRT
: ORGANISM: Porcine
US-09-841-730-14

Query Match 98.1%; Score 618; DB 9; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYSGEGCFVFLQKYPHTL 60
DB 267 DFGLCDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYSGEGCFVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 375

RESULT 9

US-09-841-730-18
; Sequence 18, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JH01470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-09-841-730-18

Query Match 98.1%; Score 618; DB 9; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYSGEGCFVFLQKYPHTL 60
DB 267 DFGLCDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYSGEGCFVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 375

RESULT 10

US-09-859-211-14
; Sequence 14, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071

; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-211-14

Query Match 98.1%; Score 618; DB 9; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYSGEGCFVFLQKYPHTL 60
DB 267 DFGLCDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYSGEGCFVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 375

RESULT 11

US-09-859-211-23
; Sequence 23, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-859-211-23

Query Match 98.1%; Score 618; DB 9; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYSGEGCFVFLQKYPHTL 60
DB 267 DFGLCDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYSGEGCFVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 375

RESULT 12

US-09-859-211-27
; Sequence 27, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:

APPLICANT: Lee, Se-jin

APPLICANT: McPherron, Alexandra C.

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8

FILE REFERENCE: 07265/144001

CURRENT APPLICATION NUMBER: US/09/859,211

CURRENT FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 09/019,070

PRIOR FILING DATE: 1998-02-05

PRIOR APPLICATION NUMBER: 08/862,445

PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 08/847,910

PRIOR FILING DATE: 1997-04-28

PRIOR APPLICATION NUMBER: 08/795,071

PRIOR FILING DATE: 1997-02-05

PRIOR APPLICATION NUMBER: 08/525,596

PRIOR FILING DATE: 1995-10-26

PRIOR APPLICATION NUMBER: PCT/US94/03019

PRIOR FILING DATE: 1994-03-18

PRIOR APPLICATION NUMBER: 08/033,923

PRIOR FILING DATE: 1993-03-19

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 27

LENGTH: 375

TYPE: PRT

ORGANISM: Meleagris gallopavo

US-09-859-211-27

Query Match

Best Local Similarity 98.1%; Score 618; DB 9; Length 375;

Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 267 DFGDCEHSTESRCRRPLTYDFAFGWDMITAPKRYKANYSGECEFVLQKYPHTL 60

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGS 109

DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGS 375

RESULT 13

US-09-859-211-29

; Sequence 29, Application US/09859211

; Patent No. US20020157125A1

; GENERAL INFORMATION:

APPLICANT: Lee, Se-jin

APPLICANT: McPherron, Alexandra C.

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8

FILE REFERENCE: 07265/144001

CURRENT APPLICATION NUMBER: US/09/859,211

CURRENT FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 09/019,070

PRIOR FILING DATE: 1998-02-05

PRIOR APPLICATION NUMBER: 08/862,445

PRIOR FILING DATE: 1997-05-23

PRIOR APPLICATION NUMBER: 08/847,910

PRIOR FILING DATE: 1997-04-28

PRIOR APPLICATION NUMBER: 08/795,071

PRIOR FILING DATE: 1997-02-05

PRIOR APPLICATION NUMBER: 08/525,596

PRIOR FILING DATE: 1995-10-26

PRIOR APPLICATION NUMBER: PCT/US94/03019

PRIOR FILING DATE: 1994-03-18

PRIOR APPLICATION NUMBER: 08/033,923

PRIOR FILING DATE: 1993-03-19

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 29

LENGTH: 375

TYPE: PRT

ORGANISM: Porcine

US-09-859-211-29

Query Match

Best Local Similarity 98.1%; Score 618; DB 9; Length 375;

Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRRPLTYDFAFGWDMITAPKRYKANYSGECEFVLQKYPHTL 60

DB 267 DFGDCEHSTESRCRRPLTYDFAFGWDMITAPKRYKANYSGECEFVLQKYPHTL 326

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGS 109

DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGS 375

RESULT 14

US-09-454-540-5

; Sequence 5, Application US/09454540

; Patent No. US20010053358A1

; GENERAL INFORMATION:

APPLICANT: Se-jin Lee and Alexandra McPherron

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: California

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/454,540

FILING DATE: 06-DEC-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/795,671

FILING DATE: February 6, 1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: HAILE, PH.D., LISA A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/106001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

IMMEDIATE SOURCE:

CLONE: GDF-8

FEATURE:

NAME/KEY: Protein

LOCATION: 1..375

US-09-454-540-5

Query Match

Best Local Similarity 98.1%; Score 618; DB 10; Length 375;

Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db      267 DFGIDCDHSTSRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFYFLQKYPHTL 326
QY      61 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 109
      |||
Db      327 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 375
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RESULT 15

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US-09-841-730-4
; Sequence 4, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; FILE REFERENCE: JH01470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-841-730-4
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Query Match      98.1%; Score 618; DB 9; Length 376;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1  DFGIDCDHSTSRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFYFLQKYPHTL 60
      |||
Db      268 DFGIDCDHSTSRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFYFLQKYPHTL 327
QY      61 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 109
      |||
Db      328 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 376
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Search completed: January 31, 2003, 18:27:18
Job time : 8 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:19:03 : Search time 17.5 Seconds

(without alignments)
501.352 Million cell updates/sec

Title: US-09-620-586B-12

Perfect score: 630
Sequence: 1 DFGIDCDHEHSTESRCRYPPL.....EGQIIYGIKIPAMVVDRCGCS 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 402399 seqs, 80492318 residues

Total number of hits satisfying chosen parameters: 402399

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA New:
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	109	US-09-620-586B-12	Sequence 12, Appl
2	630	100.0	375	US-09-620-586B-5	Sequence 5, Appl
3	630	100.0	375	US-10-251-115-2	Sequence 2, Appl
4	618	98.1	109	US-09-620-586B-11	Sequence 11, Appl
5	618	98.1	126	US-10-278-803-6	Sequence 6, Appl
6	618	98.1	126	US-10-335-483-6	Sequence 6, Appl
7	618	98.1	160	US-09-620-586B-23	Sequence 23, Appl
8	618	98.1	254	US-09-620-586B-22	Sequence 22, Appl
9	618	98.1	362	US-09-620-586B-2	Sequence 5, Appl
10	618	98.1	375	US-09-871-604A-5	Sequence 5, Appl
11	618	98.1	375	US-09-620-586B-1	Sequence 1, Appl
12	618	98.1	375	US-09-620-586B-3	Sequence 3, Appl
13	618	98.1	375	US-09-620-586B-8	Sequence 8, Appl
14	618	98.1	375	US-10-278-803-14	Sequence 14, Appl
15	618	98.1	375	US-10-278-803-19	Sequence 19, Appl
16	618	98.1	375	US-10-278-803-21	Sequence 21, Appl
17	618	98.1	375	US-10-278-803-23	Sequence 23, Appl
18	618	98.1	375	US-10-278-803-27	Sequence 27, Appl
19	618	98.1	375	US-10-251-115-8	Sequence 8, Appl
20	618	98.1	375	US-10-335-483-14	Sequence 14, Appl
21	618	98.1	376	US-09-871-604A-10	Sequence 10, Appl
22	618	98.1	376	US-09-620-586B-4	Sequence 4, Appl
23	618	98.1	376	US-09-620-586B-7	Sequence 7, Appl
24	618	98.1	376	US-10-278-803-12	Sequence 12, Appl
25	618	98.1	376	US-10-278-803-25	Sequence 25, Appl
26	618	98.1	376	US-10-251-115-6	Sequence 6, Appl

27	618	98.1	376	US-10-335-483-12	Sequence 12, Appl
28	612	97.1	375	US-09-620-586B-10	Sequence 10, Appl
29	608	96.5	375	US-09-620-586B-6	Sequence 6, Appl
30	579	91.9	108	US-10-278-803-8	Sequence 8, Appl
31	579	91.9	108	US-10-335-483-8	Sequence 8, Appl
32	573	91.0	126	US-09-871-604A-6	Sequence 6, Appl
33	573	91.0	405	US-09-871-604A-2	Sequence 2, Appl
34	573	91.0	407	US-09-871-604A-4	Sequence 4, Appl
35	559	88.7	374	US-09-620-586B-9	Sequence 9, Appl
36	540	85.7	109	US-09-620-586B-17	Sequence 17, Appl
37	522	82.9	109	US-09-620-586B-15	Sequence 15, Appl
38	519	82.4	109	US-09-620-586B-21	Sequence 21, Appl
39	518	82.2	109	US-09-620-586B-16	Sequence 16, Appl
40	510	81.0	109	US-09-620-586B-20	Sequence 20, Appl
41	504.5	80.1	128	US-09-620-586B-18	Sequence 18, Appl
42	494	78.4	109	US-09-620-586B-19	Sequence 19, Appl
43	490	77.8	109	US-09-620-586B-1	Sequence 1, Appl
44	258.5	41.0	102	US-10-072-012-831	Sequence 831, App
45	258.5	41.0	102	US-10-072-012-833	Sequence 833, App

ALIGNMENTS

RESULT 1
US-09-620-586B-12
; Sequence 12, Application US/09620586B
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620, 586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(109)
; OTHER INFORMATION: Identical to residues 267-375 in SEQ ID NO: 5
US-09-620-586B-12

Query Match 100.0%; Score 630; DB 5; Length 109;
Best local similarity 100.0%; Pred. No. 9.9e-63;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGIDCDHEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
Db 1 DFGIDCDHEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIIYGIKIPAMVVDRCGCS 109
Db 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIIYGIKIPAMVVDRCGCS 109

RESULT 2
US-09-620-586B-5
; Sequence 5, Application US/09620586B
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620, 586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Bos taurus

US-09-620-586B-5

Query Match 100.0%; Score 630; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.3e-62;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIYKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIYKIPAMVVDRCGCS 375

RESULT 3

US-10-251-115-2
; Sequence 2, Application US/10251115
; GENERAL INFORMATION:
; APPLICANT: Grobet, Luc; Georges, Michel; and Poncelet, Dominique
; TITLE OF INVENTION: MUTATIONS IN THE MYOSTATIN GENE CAUSING DOUBLE-MUSCLING IN MAMMAL
; FILE REFERENCE: 52836/00016
; CURRENT APPLICATION NUMBER: US/10/251,115
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/482,573
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 08/891,789
; PRIOR FILING DATE: 1997-07-14
; PRIOR APPLICATION NUMBER: 09/007,761
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: PCT/IB98/01197
; PRIOR FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Bos taurus
; US-10-251-115-2

Query Match 100.0%; Score 630; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.3e-62;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIYKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIYKIPAMVVDRCGCS 375

RESULT 4

US-09-620-586B-11
; Sequence 11, Application US/09620586B
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(109)
; OTHER INFORMATION: Identical to residues 267-375 in SEQ ID NO: 1
; US-09-620-586B-11

Query Match 98.1%; Score 618; DB 5; Length 109;
Best Local Similarity 98.2%; Pred. No. 2.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIYKIPAMVVDRCGCS 109
DB 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIYKIPAMVVDRCGCS 109

RESULT 5

US-10-278-803-6
; Sequence 6, Application US/10278803
; GENERAL INFORMATION:
; APPLICANT: Se-Jin Lee et al.,
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,803
; FILING DATE: 22-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,501
; FILING DATE: 30-Nov-1999
; APPLICATION NUMBER: 08/795,071
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/US94/03019
; FILING DATE: 18-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Haile, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/105001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
; US-10-278-803-6

Query Match 98.1%; Score 618; DB 6; Length 126;
Best Local Similarity 98.2%; Pred. No. 2.5e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 18 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 77

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIYKIPAMVVDRCGCS 109
DB 78 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIYKIPAMVVDRCGCS 126


```
RESULT 6
US-10-335-483-6
; Sequence 6, Application US/10335483
; GENERAL INFORMATION:
;   APPLICANT: Huynh, Thanh
;   TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
;   NUMBER OF SEQUENCES: 32
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson P.C.
;     STREET: 4225 Executive Square, Suite 1400
;     CITY: La Jolla
;     STATE: CA
;     COUNTRY: US
;     ZIP: 92037
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   OPERATING SYSTEM: Windows95
;   SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/335,483
;   FILING DATE: 31-Dec-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/177,860
;   FILING DATE: <Unknown>
;   APPLICATION NUMBER: 08/525,596
;   FILING DATE: 19-SEP-1995
;   APPLICATION NUMBER: PCT/US94/07762
;   FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Wetherell, Jr., Ph.D., John R.
;   REGISTRATION NUMBER: 31,678
;   REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 619-678-5070
;   TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 126 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     FRAGMENT TYPE: internal
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-335-483-6

Query Match          98.1%; Score 618; DB 6; Length 126;
Best Local Similarity 98.2%; Pred. No. 2.5e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTHL 60
DB 18 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTHL 77

QY 61 VHQAANRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 78 VHQAANRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 126

RESULT 7
US-09-620-586B-23
; Sequence 23, Application US/09620586B
; GENERAL INFORMATION:
;   APPLICANT: M&E Biotech A/S
;   TITLE OF INVENTION: Method for down-regulating GDF-8 activity
;   FILE REFERENCE: 3631-0117P
;   CURRENT APPLICATION NUMBER: US/09/620,586B
;   CURRENT FILING DATE: 2000-07-20
;   NUMBER OF SEQ ID NOS: 24
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
```

```
LENGTH: 160
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: MUTAGEN
LOCATION: (16)..(36)
OTHER INFORMATION: Tetanus toxoid P30 epitope (SEQ ID NO: 14)
FEATURE:
NAME/KEY: MUTAGEN
LOCATION: (37)..(51)
OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 13)
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (1)..(15)
OTHER INFORMATION: Identical to residues 216-230 of SEQ ID NO: 1
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (52)..(160)
OTHER INFORMATION: Identical to residues 267-375 of SEQ ID NO: 1
FEATURE:
NAME/KEY: SITE
LOCATION: (124)
OTHER INFORMATION: Cys or Ser
FEATURE:
NAME/KEY: SITE
LOCATION: (141)..(142)
OTHER INFORMATION: Lys Glu or Glu Gly
US-09-620-586B-23

Query Match          98.1%; Score 618; DB 5; Length 160;
Best Local Similarity 98.2%; Pred. No. 3.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTHL 60
DB 52 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTHL 111

QY 61 VHQAANRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 112 VHQAANRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 160

RESULT 8
US-09-620-586B-22
; Sequence 22, Application US/09620586B
; GENERAL INFORMATION:
;   APPLICANT: M&E Biotech A/S
;   TITLE OF INVENTION: Method for down-regulating GDF-8 activity
;   FILE REFERENCE: 3631-0117P
;   CURRENT APPLICATION NUMBER: US/09/620,586B
;   CURRENT FILING DATE: 2000-07-20
;   NUMBER OF SEQ ID NOS: 24
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: (110)..(124)
;   OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 13)
; FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: (125)..(145)
;   OTHER INFORMATION: Diptheria toxoid P30 epitope (SEQ ID NO: 14)
; FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: (1)..(109)
;   OTHER INFORMATION: 109 C-terminal residues of human and bovine GDF-8
;   FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: (146)..(254)
```

```
; OTHER INFORMATION: 109 C-terminal residues of human and bovine GDF-8
; OTHER INFORMATION: (residues 267-375 in SEQ ID NO: 1
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (90)..(91)
; OTHER INFORMATION: Lys Glu or Glu Gly
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (235)..(236)
; OTHER INFORMATION: Identical to (90)..(91)
US-09-620-586B-22
```

```
Query Match          98.1%; Score 618; DB 5; Length 254;
Best Local Similarity 98.2%; Pred. No. 4.9e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGEGCEFVFLQKYPHTL 60
DB 146 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGEGCEFVFLQKYPHTL 205
```

```
QY 61 VHOANPRGSAGPCCCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
DB 206 VHOANPRGSAGPCCCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 254
```

```
RESULT 9
US-09-620-586B-2
; Sequence 2, Application US/09620586B
; GENERAL INFORMATION:
```

```
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Melalegris gallopavo
US-09-620-586B-2
```

```
Query Match          98.1%; Score 618; DB 5; Length 362;
Best Local Similarity 98.2%; Pred. No. 6.9e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGEGCEFVFLQKYPHTL 60
DB 254 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGEGCEFVFLQKYPHTL 313
```

```
QY 61 VHOANPRGSAGPCCCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
DB 314 VHOANPRGSAGPCCCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 362
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```
RESULT 10
US-09-871-604A-5
; Sequence 5, Application US/09871604A
; GENERAL INFORMATION:
```

```
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: LEE, Se-jin
; APPLICANT: MCPHERSON, Alexandra C.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN ANIMALS EXPRESSING A GDF-11 DOMINANT NEGATIVE
; FILE REFERENCE: JHU1200-10
; CURRENT APPLICATION NUMBER: US/09/871,604A
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: US 09/123,929
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: US 09/019,901
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: US 08/795,671
; PRIOR FILING DATE: 1997-02-06
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; PRIOR APPLICATION NUMBER: US 08/706,958
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: US 08/272,763
; PRIOR FILING DATE: 1994-07-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Human GDF-8
US-09-871-604A-5
```

```
Query Match          98.1%; Score 618; DB 5; Length 375;
Best Local Similarity 98.2%; Pred. No. 7.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGEGCEFVFLQKYPHTL 60
DB 267 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGEGCEFVFLQKYPHTL 326
```

```
QY 61 VHOANPRGSAGPCCCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 375
```

```
RESULT 11
US-09-620-586B-1
; Sequence 1, Application US/09620586B
; GENERAL INFORMATION:
```

```
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-586B-1
```

```
Query Match          98.1%; Score 618; DB 5; Length 375;
Best Local Similarity 98.2%; Pred. No. 7.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGEGCEFVFLQKYPHTL 60
DB 267 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYSGEGCEFVFLQKYPHTL 326
```

```
QY 61 VHOANPRGSAGPCCCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCCTPTKMSPINMLYFNGEGQIYGIKIPAMVVDRCGCS 375
```

```
RESULT 12
US-09-620-586B-3
; Sequence 3, Application US/09620586B
; GENERAL INFORMATION:
```

```
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Gallus sp.
US-09-620-586B-3
```

```
Query Match          98.1%; Score 618; DB 5; Length 375;
```

Best Local Similarity 98.2%; Pred. No. 7.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGEGEFVFLQKYPHTL 60
|||
Db 267 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGEGEFVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNGEQIYKIPAMVVDRCGCS 109
|||
Db 327 VHOANPRGSAGPCCPTPKMSPINMLYFNGEQIYKIPAMVVDRCGCS 375

RESULT 13

US-09-620-586B-8
; Sequence 8, Application US/09620586B
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-620-586B-8

Query Match 98.1%; Score 618; DB 5; Length 375;
Best Local Similarity 98.2%; Pred. No. 7.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGEGEFVFLQKYPHTL 60
|||
Db 267 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGEGEFVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNGEQIYKIPAMVVDRCGCS 109
|||
Db 327 VHOANPRGSAGPCCPTPKMSPINMLYFNGEQIYKIPAMVVDRCGCS 375

RESULT 14

US-10-278-803-14
; Sequence 14, Application US/10278803
; GENERAL INFORMATION:
; APPLICANT: Se-jin Lee et al.,
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,803
; FILING DATE: 22-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,501
; FILING DATE: 30-Nov-1999
; APPLICATION NUMBER: 08/795,071
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/US94/03019
; FILING DATE: 18-March-1994
; ATTORNEY/AGENT INFORMATION:

NAME: Lisa A. Hallie, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/105001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-278-803-14

Query Match 98.1%; Score 618; DB 6; Length 375;
Best Local Similarity 98.2%; Pred. No. 7.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGEGEFVFLQKYPHTL 60
|||
Db 267 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGEGEFVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNGEQIYKIPAMVVDRCGCS 109
|||
Db 327 VHOANPRGSAGPCCPTPKMSPINMLYFNGEQIYKIPAMVVDRCGCS 375

RESULT 15

US-10-278-803-19
; Sequence 19, Application US/10278803
; GENERAL INFORMATION:
; APPLICANT: Se-jin Lee et al.,
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,803
; FILING DATE: 22-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,501
; FILING DATE: 30-Nov-1999
; APPLICATION NUMBER: 08/795,071
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/US94/03019
; FILING DATE: 18-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Hallie, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/105001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:

Sun Feb 2 11:34:36 2003

us-09-620-586b-12.rapn

page 6

```
; CLONE: Baboon GDF-8
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1...375
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-278-803-19
```

```
Query Match 98.1%; Score 618; DB 6; Length 375;
Best Local Similarity 98.2%; Pred. No. 7.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECFVFLQKYPHTL 60
Db 267 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECFVFLQKYPHTL 326

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
Db 327 VHQANPRGSAGPCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
```

Search completed: January 31, 2003, 18:26:55
Job time : 17.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 25 Seconds

(without alignments)
898.365 Million cell updates/sec

Title: US-09-620-586B-12

Perfect score: 630
Sequence: 1 DFGLDCEHSTESRCRCRYPL.....EGQIYGIKIPAMVVDRCGCS 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_ricent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	375	6 Q8WNS6	Q8WNS6 bos taurus
2	618	98.1	162	6 Q9T5Y2	Q9T5Y2 sus scrofa
3	618	98.1	375	6 Q9GM97	Q9GM97 equus caball
4	618	98.1	375	6 Q95D86	Q95D86 macaca fasc
5	618	98.1	375	13 Q8UWD8	Q8UWD8 columba liv
6	618	98.1	375	13 Q8UWD7	Q8UWD7 coturnix ch
7	613	97.3	375	13 Q98SP0	Q98SP0 gallus gall
8	612	97.1	375	13 Q8UWD9	Q8UWD9 anser anser
9	610	96.8	375	13 Q8UWE0	Q8UWE0 anas platyr
10	595	94.4	185	6 Q95N11	Q95N11 capra hircu
11	588	93.3	185	6 Q9M218	Q9M218 ovis aries
12	559	88.7	389	13 Q90YX0	Q90YX0 ictalurus p
13	556	88.3	385	13 Q90W05	Q90W05 sparus aur
14	553	87.8	373	13 Q90D18	Q90D18 salmo salar
15	553	87.8	373	13 Q90D22	Q90D22 oncorhynch
16	553	87.8	373	13 Q90ZD1	Q90ZD1 oncorhynch

17	553	87.8	376	13 Q98TB4	Q98TB4 oreochromis
18	553	87.8	376	13 Q90WC9	Q90WC9 morone saxa
19	553	87.8	376	13 Q90WC8	Q90WC8 morone amer
20	552	87.6	373	13 Q90W17	Q90W17 salmo salar
21	551	87.5	376	13 Q90W06	Q90W06 umbrina cir
22	548	87.0	377	13 Q98TB3	Q98TB3 morone chry
23	546	86.7	373	13 Q98UB3	Q98UB3 salvelinus
24	543	86.2	359	13 Q9W759	Q9W759 calina mos
25	532	84.4	359	13 Q8QG53	Q8QG53 sparus aur
26	521	82.7	107	6 Q9BG54	Q9BG54 sus scrofa
27	394	62.5	78	6 Q9XS86	Q9XS86 equus caball
28	311	49.4	191	13 Q98TY4	Q98TY4 perca flave
29	302	47.9	104	13 Q90Z79	Q90Z79 ictalurus p
30	299.5	47.5	598	5 Q9XZ62	Q9XZ62 drosophila
31	299.5	47.5	598	5 Q9V4F4	Q9V4F4 drosophila
32	286	45.4	58	6 Q95MF3	Q95MF3 sus scrofa
33	259	41.1	263	13 Q8QH11	Q8QH11 umbrina cir
34	257	40.8	370	13 Q91350	Q91350 xenopus lae
35	245	38.9	395	13 Q9PWG6	Q9PWG6 anguilla ja
36	244.5	38.8	115	13 Q9DGE9	Q9DGE9 cyprinus ca
37	244.5	38.8	393	13 Q90261	Q90261 brachydanio
38	243.5	38.7	392	13 Q9PWR8	Q9PWR8 carassius a
39	242.5	38.5	115	13 Q9DGF1	Q9DGF1 cyprinus ca
40	242.5	38.5	115	13 Q9DGF0	Q9DGF0 cyprinus ca
41	242.5	38.5	115	13 Q9DGE6	Q9DGE6 oryzias lat
42	239.5	38.0	138	13 Q9W6T9	Q9W6T9 brachydanio
43	233.5	37.1	354	13 Q9YGV1	Q9YGV1 xenopus lae
44	231.5	36.7	349	5 Q97138	Q97138 brugia mala
45	223.5	35.5	361	5 Q96504	Q96504 branchiosto

ALIGNMENTS

RESULT 1
Q8WNS6 ID Q8WNS6 PRELIMINARY; PRT; 375 AA.

AC Q8WNS6; ID Q8WNS6; PRELIMINARY; PRT; 375 AA.
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Myostatin.
GN GDF8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Shibata M., Muramoto T., Aikawa K.;
RT "Genomic organization and sequence of the myostatin gene in bovine.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB076403; BAB79498.1; -
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00016; EF_HAND; UNKNOWN 1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN 1.
SQ SEQUENCE 375 AA; 42524 MW; 0EC27616C202F5E6 CRC64;

Query Match 100.0%; Score 630; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.6e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYSGECEFVLQKYPTHTL 60
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYSGECEFVLQKYPTHTL 326

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 375

RESULT 2

Q9TSY2 PRELIMINARY; PRT; 162 AA.
AC Q9TSY2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN MSTN.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20078370; PubMed=10612246;
RA Stratil A., Kopecky M.;
RT "Genomic organization, sequence and polymorphism of the porcine
RT myostatin (GDF8; MSTN) gene."
RL Anim. Genet. 30:468-470(1999).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AJ237920; CAB40844.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGFb_N.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
FT NON TER
SQ SEQUENCE 162 AA; 18290 MW; FE3535334512856E CRC64;

Query Match 98.1%; Score 618; DB 6; Length 162;
Best Local Similarity 98.2%; Pred. No. 2.8e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVFLQKYPHTL 60
DB 54 DFGLCDDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVFLQKYPHTL 113
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 109
DB 114 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 162

RESULT 3

Q9GM97 PRELIMINARY; PRT; 375 AA.
AC Q9GM97;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=THROUGHBRED;
RA Hosoyama T., Yamanouchi K., Tojo H., Tachi C.;
RT "Molecular cloning of equine myostatin cDNA and serum level of
RT myostatin in horse.";

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AB033541; BAB16046.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb_N.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42736 MW; 6FA24ECBEE4D9936 CRC64;

Query Match 98.1%; Score 618; DB 6; Length 375;
Best Local Similarity 98.2%; Pred. No. 6.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVFLQKYPHTL 60
DB 267 DFGLCDDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 375

RESULT 4

Q95J86 PRELIMINARY; PRT; 375 AA.
AC Q95J86;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Myostatin.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GASTROCNEMUS;
RA Smock S.L., Owen T.A.;
RT "Cloning of the open reading frame DNA for macaque fascicularis
RT (cynomolgus macaque) myostatin (GDF8).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AY055750; AAL17640.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb_N.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42722 MW; 2149B46AC7D446E7 CRC64;

Query Match 98.1%; Score 618; DB 6; Length 375;
Best Local Similarity 98.2%; Pred. No. 6.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVFLQKYPHTL 60
DB 267 DFGLCDDEHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 375

RESULT 5

Q8UWD8 PRELIMINARY; PRT; 375 AA.

AC Q8UWD8; 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Myostatin.
GN MSTN.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440863; AAL35277.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42739 MW; 88296F0AE779476E CRC64;

Query Match 98.1%; Score 618; DB 13; Length 375;
Best Local Similarity 98.2%; Pred. No. 6.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIAPKRYKANYSGECEVFLOKYPHTL 60
D 267 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIAPKRYKANYSGECEVFLOKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKSPINMLYFNGEQIYGIKIPAMVVDRCGCS 109
D 327 VHQANPRGSAGPCTPTKSPINMLYFNGEQIYGIKIPAMVVDRCGCS 375

RESULT 6

Q8UWD7 PRELIMINARY; PRT; 375 AA.

AC Q8UWD7; 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Myostatin.
GN MSTN.
OS Coturnix chinensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=46218;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440864; AAL35278.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42721 MW; B893B1IA42DE0725 CRC64;

Query Match 98.1%; Score 618; DB 13; Length 375;
Best Local Similarity 98.2%; Pred. No. 6.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIAPKRYKANYSGECEVFLOKYPHTL 60
D 267 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIAPKRYKANYSGECEVFLOKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKSPINMLYFNGEQIYGIKIPAMVVDRCGCS 109
D 327 VHQANPRGSAGPCTPTKSPINMLYFNGEQIYGIKIPAMVVDRCGCS 375

RESULT 7

Q98SP0 PRELIMINARY; PRT; 375 AA.

AC Q98SP0; 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Myostatin.
GN MSTN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Yang W., Zhu D.;
RT "Genomic structure and expression of the chicken GDF-8 during
RT development."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF346599; AAK18000.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42717 MW; D980E286426E4D4F CRC64;

Query Match 97.3%; Score 613; DB 13; Length 375;
Best Local Similarity 97.2%; Pred. No. 2.5e-63;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIAPKRYKANYSGECEVFLOKYPHTL 60
D 267 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIAPKRYKANYSGECEVFLOKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKSPINMLYFNGEQIYGIKIPAMVVDRCGCS 109
D 327 VHQANPRGSAGPCTPTKSPINMLYFNGEQIYGIKIPAMVVDRCGCS 375

RESULT 8

Q8UWD9 PRELIMINARY; PRT; 375 AA.

AC Q8UWD9; 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)


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DE Myostatin.
GN MSTN.
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8843;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440862; AAL35276.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SMO0204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42667 MW; 57DDE49D3AA2978C CRC64;

Query Match 97.1%; Score 612; DB 13; Length 375;
Best Local Similarity 97.2%; Pred. No. 3.3e-63;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGLCDHEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVLQKYPHTL 60
DB 267 DFGLCDHEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCFGECEFFVLQKYPHTL 326

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 375

RESULT 9
Q8UWE0 PRELIMINARY; PRT; 375 AA.
AC Q8UWE0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440861; AAL35275.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SMO0204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42817 MW; 1BA7FF5225C23620 CRC64;

Query Match 96.8%; Score 610; DB 13; Length 375;
Best Local Similarity 97.2%; Pred. No. 5.6e-63;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGLCDHEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVLQKYPHTL 60
DB 267 DFGLCDHEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCFGECEFFVLQKYPHTL 326
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DB 267 DFGLCDHEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVLQKYPHTL 326

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCGCS 375

RESULT 10
Q95N11 PRELIMINARY; PRT; 185 AA.
AC Q95N11;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN MSTN.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Lian Z., Pan Q., Chen H., Jin H., Li N.;
RT "Cloning of Intron 2 of the myostatin gene in goat.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AY032689; AAK49790.1; -.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
FT NON_TER 1
FT NON_TER 185
SQ SEQUENCE 185 AA; 20953 MW; 03675B386E9D64D4 CRC64;

Query Match 94.4%; Score 595; DB 6; Length 185;
Best Local Similarity 95.3%; Pred. No. 1.5e-61;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGLCDHEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVLQKYPHTL 60
DB 79 DFGLCDHEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCSGCEFFVLQKYPHTL 138

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCG 107
DB 139 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEQIITYGKIPAMVVDRCG 185

RESULT 11
Q9MZ18 PRELIMINARY; PRT; 185 AA.
AC Q9MZ18;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN MSTN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Lian Z., Jin H., Li N.;
RT "Cloning of Intron 2 of the myostatin gene in sheep.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF266758; AAF78069.1; -.
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DR H5SP; P12643; 3BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT NON_TER 185 185
SQ SEQUENCE 185 AA; 20923 MW; BA9634203A552850 CRC64;

Query Match 93.3%; Score 588; DB 6; Length 185;
Best Local Similarity 94.4%; Pred. No. 1e-60;
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLOKYPHTL 60
DB 79 DFGLCDVHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLOKYPHTL 138
OY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCG 107
DB 139 VHQANPKGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCG 185

RESULT 12

O90YY0 PRELIMINARY; PRT; 389 AA.

AC O90YY0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Myostatin.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Kocabas A.M., Liu Z.J.;
RT "Molecular characterization and expression of the myostatin gene from channel catfish (Ictalurus punctatus).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF396747; AAK8466.1; -.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 389 AA; 43600 MW; 569FB952B7E9E173 CRC64;

Query Match 88.7%; Score 559; DB 13; Length 389;
Best Local Similarity 88.8%; Pred. No. 5.2e-57;
Matches 95; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

OY 3 GUDCDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLOKYPHTL 62
DB 283 GUDCDENSSSRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLOKYPHTL 342
OY 63 QANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 343 KANPRGTAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 389

RESULT 13

O90W05 PRELIMINARY; PRT; 385 AA.
AC O90W05;

DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Myostatin.
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RA Maccatrozzo L., Bargelloni L., Radaelli G., Mascarello F.,
RA Patarnello T.;
RT "Characterization of the myostatin gene in the gilthead seabream, Sparus aurata: sequence, genomic structure, and expression pattern.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF258446; AAK53545.1; -.
DR EMBL; AF258447; AAK53544.1; -.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 385 AA; 43704 MW; 18F902CE325A3916 CRC64;

Query Match 88.3%; Score 556; DB 13; Length 385;
Best Local Similarity 88.1%; Pred. No. 1.1e-56;
Matches 96; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

OY 1 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLOKYPHTL 60
DB 277 DFGLCDENSSSRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEFFVLOKYPHTL 336
OY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 337 VHKANPRGSAGPCCTPTKMSPINMLYFNRKEQIIYGKIPAMVVDRCGCS 385

RESULT 14

O9DD18 PRELIMINARY; PRT; 373 AA.

AC O9DD18;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Myostatin precursor.
GN GDF-8.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.;
RT "The two myostatin genes of Atlantic salmon (Salmo salar) are expressed in a variety of tissues.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Andersen O.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.,
RA Andersen O.;
RT "The two myostatin genes of Atlantic salmon (Salmo salar) are expressed in a variety of tissues.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

Job time : 25 secs

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AJ297267; CAC19541.2; ~.
DR EMBL; AJ316006; CAC59700.1; ~.
DR HSSP; P12643; 3BP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 265 373 MYOSTATIN.
SQ SEQUENCE 373 AA; 41896 MW; C641D71D83E66C4D CRC64;

Query Match 87.8%; Score 553; DB 13; Length 373;
Best Local Similarity 87.2%; Pred. No. 2.5e-56;
Matches 95; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECEFFVFLQKYPHTL 60
DB 265 DSGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECEFFVFLQKYPHTL 324
QY 61 VHQANPRGSAGPCTPTKMSPINMLYENGEGQIIYGKIPAMVVDRCGCS 109
DB 325 VNKANPRGTAGPCTPTKMSPINMLYFNKKEQIIYGKIPSMVVDRCGCS 373

RESULT 15

Q90ZD2 PRELIMINARY; PRT; 373 AA.
ID Q90ZD2;
AC Q90ZD2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Myostatin 1.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_Taxid=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Rescan P.-Y.; Jutel I.; Ralliere C.;
RT "Two myostatin genes are differentially expressed in myotomal muscle
of the trout (Oncorhynchus mykiss).";
RL J. Exp. Biol. 0:0-0(2001).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF273035; AAK71707.1; ~.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 373 AA; 42049 MW; 9DD4771B5CF671EA CRC64;

Query Match 87.8%; Score 553; DB 13; Length 373;
Best Local Similarity 87.2%; Pred. No. 2.5e-56;
Matches 95; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECEFFVFLQKYPHTL 60
DB 265 DSGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECEFFVFLQKYPHTL 324
QY 61 VHQANPRGSAGPCTPTKMSPINMLYENGEGQIIYGKIPAMVVDRCGCS 109
DB 325 VNKANPRGTAGPCTPTKMSPINMLYFNKKEQIIYGKIPSMVVDRCGCS 373

Search completed: January 31, 2003, 18:21:08

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 8.5 Seconds
(without alignments)
531.873 Million cell updates/sec

Title: US-09-620-586b-12
Perfect score: 630
Sequence: 1 DFGLDDEHSTESRCRYP...EGQIYKIPAMVVDRCGS 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	length	ID	Description
1	630	100.0	375	1	GDF8_BOVIN
2	618	98.1	375	1	GDF8_CHICK
3	618	98.1	375	1	GDF8_HUMAN
4	618	98.1	375	1	GDF8_MELGA
5	618	98.1	375	1	GDF8_PIG
6	618	98.1	376	1	GDF8_MOUSE
7	618	98.1	376	1	GDF8_RAT
8	612	97.1	375	1	GDF8_PAPHA
9	608	96.5	375	1	GDF8_SHEEP
10	573	91.0	405	1	GDF8_MOUSE
11	573	91.0	407	1	GDF8_HUMAN
12	559	88.7	374	1	GDF8_BRARE
13	526	83.5	345	1	GDF8_RAT
14	251	39.8	255	1	IHBB_MOUSE
15	246	39.0	391	1	IHBB_CHICK
16	245	38.9	349	1	IHBB_PIG
17	245	38.9	407	1	IHBB_HUMAN
18	245	38.9	408	1	IHBB_BOVIN
19	243	38.6	355	1	DVRI_BRARE
20	232.5	36.9	207	1	BMP6_RAT
21	232.5	36.9	513	1	BMP6_HUMAN
22	230.5	36.6	510	1	BMP6_MOUSE
23	219.5	34.8	426	1	IHBA_HORSE
24	219	34.8	350	1	DAF7_CAEEL
25	218.5	34.7	125	1	GDF6_MOUSE
26	218.5	34.7	436	1	GDF6_BOVIN
27	216.5	34.4	352	1	IHBC_MOUSE
28	216.5	34.4	360	1	DVRI_XENLA
29	214.5	34.0	426	1	BMP7_XENLA
30	213.5	33.9	424	1	IHBA_MOUSE
31	213.5	33.9	424	1	IHBA_PIG
32	213.5	33.9	424	1	IHBA_RAT
33	213.5	33.9	425	1	IHBA_BOVIN

34	213.5	33.9	425	1	IHBA_SHEEP	P43032	ovis aries
35	213.5	33.9	426	1	IHBA_HUMAN	P08476	homo sapien
36	212.5	33.7	350	1	IHBE_MOUSE	O08717	mus musculu
37	212.5	33.7	350	1	IHBE_RAT	O08959	rattus norv
38	212.5	33.7	402	1	BMP8_HUMAN	P34820	homo sapien
39	212.5	33.7	431	1	GDF7_MOUSE	P18075	homo sapien
40	211.5	33.6	151	1	GDF7_MOUSE	P43029	mus musculu
41	211.5	33.6	350	1	IHBE_HUMAN	P58166	homo sapien
42	211.5	33.6	352	1	IHBC_HUMAN	P55103	homo sapien
43	210.5	33.4	430	1	BMP7_MOUSE	P23359	mus musculu
44	210.5	33.4	495	1	GDF5_MOUSE	P43027	mus musculu
45	210.5	33.4	501	1	GDF5_HUMAN	P43026	homo sapien

ALIGNMENTS

RESULT 1
ID GDF8_BOVIN STANDARD; PRT; 375 AA.
AC 018836; 018829; Q95N97;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN OR MH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT MH TYR-313.
RC STRAIN=Friesian; TISSUE=Muscle, and Embryo;
RX MEDLINE=97458167; PubMed=9314496;
RA Kambadur R., Sharma M., Smith T.P.L., Bass J.J.;
RT "Mutations in myostatin (GDF8) in double-muscled Belgian Blue and
Piedmontese cattle.";
RL Genome Res. 7:910-916(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS MH LEU-94 AND TYR-313.
RC STRAIN=Holstein; TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-U.;
RT "Double musculing in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21343337; PubMed=11451380;
RA Jeanplong F., Sharma M., Somers W.G., Bass J.J., Kambadur R.;
RT "Genomic organization and neonatal expression of the bovine myostatin
gene.";
RL Mol. Cell. Biochem. 220:31-37(2001).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING AND ADULT
SKELETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIMB MUSCLES
M.SEMIMEMBRANOSUS AND M.BICEPS FEMORIS; LOW LEVELS IN OTHER
HINDLIMB MUSCLES.
CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED THROUGHOUT DEVELOPMENT.
LOW LEVELS ARE FOUND UP TO DAY 29 EMBRYOS. LEVELS INCREASE FROM
DAY 31 UP UNTIL LATE GESTATION.
CC -1- DISEASE: DEFECTS IN GDF8 ARE THE CAUSE OF THE DOUBLE-MUSCLE
PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIVE
DISEASE FREQUENTLY FOUND IN THE BELGIAN BLUE AND PIEDMONTSE
CATTLE BREEDS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED
NUMBER OF MUSCLE FIBERS (HYPERPLASIA), RESULTING IN AN INCREASE IN
MUSCLE MASS OF 20-25%.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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DR EMBL; AF019761; AAB81508.1; -
DR EMBL; AF019620; AAB86687.1; -
DR EMBL; AF320998; AAG48116.1; -
DR HSSP; P18075; IBMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Growth factor; Cytokine; Glycoprotein; Signal; Disease mutation.
FT SIGNAL 1 18
FT PROPEP 19 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 339
FT CARBOHYD 47 47
FT CARBOHYD 71 71
FT VARIANT 94 94
FT VARIANT 313 313
FT CONFLICT 14 14
SQ SEQUENCE 375 AA; 42551 MW; 84E1AB20650C05F6 CRC64;

Query Match 100.0%; Score 630; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.3e-63;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGECFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 375

RESULT 2

GDF8_CHICK STANDARD; PRT; 375 AA.
ID GDF8_CHICK
AC 042220;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
DE -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).

DR EMBL; AF019621; AAB86688.1; -
DR HSSP; P18075; IBMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 339
FT CARBOHYD 71 71
SQ SEQUENCE 375 AA; 42707 MW; DA732DB9426E4D4F CRC64;

Query Match 98.1%; Score 618; DB 1; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.2e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGECFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 375

RESULT 3

GDF8_HUMAN STANDARD; PRT; 375 AA.
ID GDF8_HUMAN
AC 014753;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=99061972; PubMed=9843994;
RA Gonzalez-Cadavid N.F., Taylor W.E., Yarasheski K., Sinha-Hikim I.,
RA Ma K., Ezat S., Shen R., Lalani R., Asa S., Mamita M., Nair G.,
RA Arver S., Bhasin S.;
RT "Organization of the human myostatin gene and expression in healthy
RT men and HIV-infected men with muscle wasting.";
RT Proc. Natl. Acad. Sci. U.S.A. 95:14938-14943(1998).
DE -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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EMBL; AF019623; AAB86690.1; -
EMBL; AF188635; AAF02770.1; -
EMBL; AF188636; AAF02771.1; -
EMBL; AF188637; AAF02772.1; -
EMBL; AF188638; AAF02773.1; -
EMBL; AF033855; AAC08035.1; -
EMBL; AF093798; AAC62489.1; -
HSSP; P18075; 1BMP.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFb; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
KW SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 266 POTENTIAL.
FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 281 340 BY SIMILARITY.
FT DISULFID 309 372 BY SIMILARITY.
FT DISULFID 313 374 BY SIMILARITY.
FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 375 AA; 42791 MW; 0F658685EFD3418 CRC64;

Query Match 98.1%; Score 618; DB 1; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.2e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWITAPKRYKANYCSGECEVFLOKYPHTL 60
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWITAPKRYKANYCSGECEVFLOKYPHTL 326
QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 375

RESULT 6
GDF8_MOUSE
ID_GDF8_MOUSE STANDARD; PRT; 376 AA.
AC 008689;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Skeletal muscle;
RX MEDLINE=97284412; PubMed=9139826;
RA McPherron A.C., Lawler A.M., Lee S.-J.;
RT "Regulation of skeletal muscle mass in mice by a new TGF-beta
superfamily member."
RL Nature 387:83-90(1997).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
MUSCLE GROWTH.

```
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT
CC SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-CONITUM IN
CC ONE-THIRD OF DEVELOPING SOMITES. AT DAY 10.5, EXPRESSED IN THE
CC MYOTOME COMPARTMENT OF SOMITES. AT LATER STAGES OF DEVELOPMENT,
CC DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION
CC CONTINUES IN ADULTHOOD.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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```

EMBL; U84005; AAC53167.1; -
HSSP; P18075; 1BMP.
MGD; MGI:95691; Gdf8.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFb; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein; Signal.
KW SIGNAL 1 24 POTENTIAL.
FT PROPEP 25 267 POTENTIAL.
FT CHAIN 268 376 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 282 341 BY SIMILARITY.
FT DISULFID 310 373 BY SIMILARITY.
FT DISULFID 314 375 BY SIMILARITY.
FT DISULFID 340 340 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 376 AA; 42921 MW; 3E19814DD62C08BE CRC64;

Query Match 98.1%; Score 618; DB 1; Length 376;
Best Local Similarity 98.2%; Pred. No. 1.2e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWITAPKRYKANYCSGECEVFLOKYPHTL 60
DB 268 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWITAPKRYKANYCSGECEVFLOKYPHTL 327
QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 109
DB 328 VHOANPRGSAGPCTPTKMSPINMLYFNGEGQIYKIPAMVVDRCGCS 376

RESULT 7
GDF8_RAT
ID_GDF8_RAT STANDARD; PRT; 376 AA.
AC 035312;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene."
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL

```
CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF019624; AAB86691.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 24
FT PROPEP 25 267
FT CHAIN 268 376
FT DISULFID 282 341
FT DISULFID 310 373
FT DISULFID 314 375
FT DISULFID 340 340
FT CARBOHYD 72
SQ SEQUENCE 376 AA; 42829 MW; 933043D8C8C3294B CRC64;

Query Match 98.1%; Score 618; DB 1; Length 376;
Best Local Similarity 98.2%; Pred. No. 1,2e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECFVFLQKYPHTL 60
DB 268 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECFVFLQKYPHTL 327

QY 61 VHQANPRGSAGCCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 328 VHQANPRGSAGCCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 376

RESULT 8
GDF8_PAPHA STANDARD; PRT; 375 AA.
ID GDF8_PAPHA
AC 018828;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C.; Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF019619; AAB86686.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 339
FT CARBOHYD 71
SQ SEQUENCE 375 AA; 42688 MW; 7B49B90ACAB9226EA CRC64;

Query Match 97.1%; Score 612; DB 1; Length 375;
Best Local Similarity 97.2%; Pred. No. 5.4e-61;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECFVFLQKYPHTL 326

QY 61 VHQANPRGSAGCCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGCCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 375

RESULT 9
GDF8_SHEEP STANDARD; PRT; 375 AA.
ID GDF8_SHEEP
AC 018830;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C.; Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
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DR EMBL; AF019622; AAB86689.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; signal.
FT SIGNAL 1 23
FT PROPEP 24 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 339
FT CARBOHYD 48 48
FT CARBOHYD 71 71
SQ SEQUENCE 375 AA; 42827 MW; 1C36F3833B11241 CRC64;

Query Match 96.5%; Score 608; DB 1; Length 375;
Best Local Similarity 95.4%; Pred. No. 1.5e-60;
Matches 104; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 267 DFGLCDDEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 375

RESULT 10
GDFB_MOUSE STANDARD; PRT; 405 AA.
ID GDFB_MOUSE
AC Q9ZIW4; Q9QX55; Q9R221;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein
DE 11).
GN GDF11 OR BMP11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99177155; PubMed=10075854;
RA Gamber L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
RA Rosen V.;
RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail
RT bud is a potent mesoderm inducer in Xenopus embryos.";
RL Dev. Biol. 208:222-232(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=99318097; PubMed=10391213;
RA McPherron A.C., Lawler A.M., Lee S.-J.;
RT "Regulation of anterior/posterior patterning of the axial skeleton by
RT growth/differentiation factor 11.";
RL Nat. Genet. 22:260-264(1999).
RN [3]
RP SEQUENCE OF 75-405 FROM N.A.
RX MEDLINE=99173787; PubMed=10072786;
RA Nakashima M., Toyono T., Akamine A., Joyner A.;
RT "Expression of growth/differentiation factor 11, a new member of the
RT BMP/TGFbeta superfamily during mouse embryogenesis.";
RL Mech. Dev. 80:185-189(1999).
CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
CC IDENTIFY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
```

```
CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD,
CC INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING
CC TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT
CC DENTAL PULP AND BRAIN.
CC -1- DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED
CC DOMAINS AT 8.5 DAYS POST COITUS (DPC) WHERE IT IS HIGHEST IN THE
CC TAIL BUD, AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB
CC BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED
CC IN TERMINALLY-DIFFERENTIATED ODONTOBLASTS, THE NASAL EPITHELIUM,
CC RETINA AND SPECIFIC REGIONS OF THE BRAIN.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF100906; AAC72853.1; -.
DR EMBL; AF100904; AAC72853.1; JOINED.
DR EMBL; AF100905; AAC72853.1; JOINED.
DR EMBL; AF028337; AAF21633.1; -.
DR EMBL; AF028335; AAF21633.1; JOINED.
DR EMBL; AF028336; AAF21633.1; JOINED.
DR HSSP; P18075; 1BMP.
DR MGD; MGI:1338027; Gdf11.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; signal.
FT SIGNAL 1 20
FT PROPEP 21 296
FT CHAIN 297 405
FT DOMAIN 29 39
FT DOMAIN 208 213
FT DISULFID 311 370
FT DISULFID 339 402
FT DISULFID 343 404
FT DISULFID 369 369
FT CARBOHYD 92 92
FT CARBOHYD 75 75
FT CONFLICT 171 171
SQ SEQUENCE 405 AA; 44946 MW; A7AE382710A14781 CRC64;

Query Match 91.0%; Score 573; DB 1; Length 405;
Best Local Similarity 89.0%; Pred. No. 1.3e-56;
Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 297 NUGLCDDEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 356

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 109
DB 357 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYKIPAMVVDRCGCS 405

RESULT 11
GDFB_HUMAN STANDARD; PRT; 407 AA.
ID GDFB_HUMAN
AC Q95390; Q9UID1; Q9UID2;
DT 16-OCT-2001 (Rel. 40, Created)
```


DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein 11).
 GN GDF11 OR BMP11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal Brain;
 RX MEDLINE=99177155; PubMed=10075854;
 RA Gerner L.W., Wolftman N.M., Celeste A.J., Hattersley G., Hewick R., Rosen V.;
 RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail bud is a potent mesoderm inducer in *Xenopus* embryos.";
 RL Dev. Biol. 208:222-232(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99318097; PubMed=10391213;
 RA McPherron A.C., Lawler A.M., Lee S.-J.;
 RT "Regulation of anterior/posterior patterning of the axial skeleton by growth/differentiation factor 11.";
 RL Nat. Genet. 22:260-264(1999).
 CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
 CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----
 CC EMBL; AF100907; AAC72852.1; -.
 DR EMBL; AF028333; AAF21630.1; -.
 DR EMBL; AF028334; AAF21631.1; -.
 DR HSSP; P18075; 1BMP.
 DR Genew; HGNC:4216; GDF11.
 DR MIM; 603936; -.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Growth factor; Cytokine; Glycoprotein; Signal.
 KM Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT PROPEP 25 298
 FT CHAIN 299 407
 FT DOMAIN 29 41
 FT DOMAIN 210 215
 FT DISULFID 313 372
 FT DISULFID 341 404
 FT DISULFID 345 406
 FT DISULFID 371 371
 FT CARBOHYD 94 94
 FT SEQUENCE 407 AA; 45090 MW; E8FF48E363635BA8 CRC64;
 SQ
 Query Match 91.0%; Score 573; DB 1; Length 407;
 Best Local Similarity 89.0%; Pred. No. 1.3e-56;
 Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 299 NLGLDDEHSESRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEYMFNOKYPHTL 358
 Oy 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGEQIYGIKIPAMVVDRCGS 109
 Db 359 VQGANPRGSAGPCCPTPTKMSPINMLYFNDKQIYGIKIPAMVVDRCGS 407
 RESULT 12
 GDF8_BRAE STANDARD; PRT; 374 AA.
 ID GDF8_BRAE
 AC 042222;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 GN GDF8 OR MSTN.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=98024153; PubMed=9356471;
 RA McPherron A.C., Lee S.-J.;
 RT "Double muscling in cattle due to mutations in the myostatin gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----
 CC EMBL; AF019626; AAB86693.1; -.
 DR HSSP; P18075; 1BMP.
 DR ZFIN; ZDB-GENE-990415-165; gdf8.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Growth factor; Cytokine; Glycoprotein; Signal.
 KM Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT PROPEP 23 265
 FT CHAIN 266 374
 FT DISULFID 280 339
 FT DISULFID 308 371
 FT DISULFID 312 373
 FT DISULFID 338 338
 FT CARBOHYD 72 72
 FT CARBOHYD 274 274
 FT SEQUENCE 374 AA; 42060 MW; 6302BC6C86562576 CRC64;
 SQ
 Query Match 88.7%; Score 559; DB 1; Length 374;
 Best Local Similarity 86.2%; Pred. No. 4.5e-55;
 Matches 94; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Db 326 VNKASPRGTAGPCTPTKMSPINMLYFNKEQIYGIKIPSWVDRGCS 374

RESULT 13

ID GDFB_RAT STANDARD; PRT; 345 AA.

AC 092217;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein 11) (Fragment).

GN GDF11 OR BMP11.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Dental pulp;

RX MEDLINE=99173787; PubMed=10072786;

RA Nakashima M., Toyono T., Akamine A., Joyner A.;

RT "Expression of growth/differentiation factor 11, a new member of the BMP/TGFbeta superfamily during mouse embryogenesis.";

RL Mech. Dev. 80:185-189(1999).

CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL

CC IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.

CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL

CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN (BY SIMILARITY).

CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

CC -----

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; AF092733; AAD05266.1; -.

DR HSSP; P18075; 1BMP.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001111; TGFb_N.

DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb_propeptide; 1.

DR Prodom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

DR Growth factor; Cytokine; Glycoprotein.

KW NON TER

FT PROPEP

FT CHAIN

FT DOMAIN

FT DISULFID

FT DISULFID

FT CARBOHYD

FT NON TER

SQ SEQUENCE

Query Match

Best Local Similarity

Matches

90; Conservative

7; Mismatches

6; Indels

0; Gaps

0;

83.5%; Score 526; DB 1; Length 345;

87.4%; Pred. No. 2e-51;

Matches

90; Conservative

7; Mismatches

6; Indels

0; Gaps

0;

1 DFGIDCDHSTSRCCRYPLTVDFEAFGWDWIAPKRYKANYCSGCEGFVFLQKYPHTL 60

243 NLGLDCDEHSSSRCCRYPLTVDFEASGWDWIAPKRYKANYCSGCEYMFQKYPHTL 302

61 VHQANPRGSAGPCCPTPKMSPINMLYFNKEQIYGIKIPAMV 103

303 VQGANPRGSAGPCCPTPKMSPINMLYFNKEQIYGIKIPAMV 345

Db

RESULT 14

ID INHB_MOUSE STANDARD; PRT; 255 AA.

AC 004999; 061277;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).

GN INHB.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE OF 1-234 FROM N.A.

RC STRAIN=CBA X NMRL; TISSUE=Testis;

RX MEDLINE=95344997; PubMed=7619733;

RA Ritvos O., Tuuri T., Eramaa M., Sainio K., Hilden K., Saxen L.,

RA Gilbert S.;

RT "Activin disrupts epithelial branching morphogenesis in developing

RT glandular organs of the mouse.";

RL Mech. Dev. 50:229-245(1995).

RN [2]

RP SEQUENCE OF 134-255 FROM N.A.

RX MEDLINE=93321614; PubMed=8330535;

RA Albano P.M., Grome N., Smith J.C.;

RT "Activins are expressed in preimplantation mouse embryos and in ES

RT and EC cells and are regulated on their differentiation.";

RL Development 117:711-723(1993).

CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.

CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE

CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,

CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,

CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,

CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR

CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPOSE THE FUNCTIONS OF

CC ACTIVINS.

CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

CC ACTIVIN A IS A HOMODIMER OF BETA-A.

CC ACTIVIN B IS A HOMODIMER OF BETA-B.

CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.

CC -1- TISSUE SPECIFICITY: UTERUS, TESTIS, OVARY, LUNG, KIDNEY, BRAIN,

CC C37 EMBRYONIC STEM CELLS, AND POSSIBLY IN LIVER.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

CC -----

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CC -----

CC EMBL; X83376; CAA58290.1; -.

DR EMBL; X69620; CAA49326.1; -.

DR PIR; S31441; S31441.

DR HSSP; P12643; 3BMP.

DR MGD; MGI:96571; Inhb.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001111; TGFb_N.

DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb_propeptide; 1.

DR Prodom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

DR Growth factor; Hormone; Glycoprotein.

KW NON TER

FT PROPEP

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT CHAIN

FT DISULFID 144 152 BY SIMILARITY.
FT DISULFID 151 220 BY SIMILARITY.
FT DISULFID 180 252 BY SIMILARITY.
FT DISULFID 184 254 BY SIMILARITY.
FT DISULFID 219 219 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 135 135 H -> D (IN REF. 2).
SQ SEQUENCE 255 AA; 29178 MW; 2524B21DC648D9A9 CRC64;

Query Match 39.8%; Score 251; DB 1; Length 255;
Best Local Similarity 44.1%; Pred. No. 7.5e-21;
Matches 52; Conservative 16; Mismatches 36; Indels 14; Gaps 6;

OY 3 GLDCDEHSTESRCRCRYPLTVDFEAFGW-DWIAPKRYKANYCSGCEGFVFLQKYP----- 56
DB 141 GLECDGRT--SLCCRQGFYIDFRLIGMNDWIAPTYGNYCEGSCP-AYLAGVPSASS 197
OY 57 -HTHLVHQANPRG-SAGP---CCTPTKSPINMLYFNGEGQIYIGKIPAMVVDRCGS 109
DB 198 FHTAVVQYRMRLNPGVNSCCIPFKLSMSMLYFDDEYNIVKRDVPMNIVEECGCA 255

RESULT 15
IHBB CHICK STANDARD; PRT; 391 AA.
AC P27093; 073796;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin beta B chain precursor (Activin beta-B chain).
GN INHBB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Follicle;
RA Klingner H., Halaschek-Wiener J., Wohlrab B.K., Kuchler K., Wohlrab F.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Ovary;
RA Hecht D.J., Davis A.J., Ryan I.M., Johnson P.A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 311-381 FROM N.A.
RX MEDLINE=91029482; PubMed=2225063;
RA Mitrani E., Ziv T., Thomsen G., Shimoni Y., Melton D.A., Brill A.;
RT "Activin can induce the formation of axial structures and is expressed
in the hypoblast of the chick."
RL Cell 63:495-501(1990).
CC -1- FUNCTION: INHIBING AND ACTIVATING INHIBIT AND ACTIVATE,
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBING/ACTIVATING ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBING APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A HOMODIMER OF BETA-A.
CC ACTIVIN B IS A HOMODIMER OF BETA-B.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL; Z71594; CAA96248.1; -.
CC EMBL; AF055478; AAC14187.1; -.
CC EMBL; M61166; AAA48568.1; -.
CC EMBL; M57408; AAA03079.1; -.
CC HSSP; P18075; 1BMP.
CC InterPro; IPR002400; GF_cysknot.
CC InterPro; IPR001839; TGFb.
CC InterPro; IPR001111; TGFb N.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGFb_propeptide; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC ProDom; PD000357; TGFb; 1.
CC SMART; SM00204; TGFb; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT PROPEP 26 276 POTENTIAL.
FT CHAIN 277 391 INHIBIN BETA B CHAIN.
FT DISULFID 280 288 BY SIMILARITY.
FT DISULFID 287 356 BY SIMILARITY.
FT DISULFID 316 388 BY SIMILARITY.
FT DISULFID 320 390 BY SIMILARITY.
FT DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 30 30 P -> PG (IN REF. 2).
SQ SEQUENCE 391 AA; 43608 MW; 060017BF33F7AF6C CRC64;

Query Match 39.0%; Score 246; DB 1; Length 391;
Best Local Similarity 41.5%; Pred. No. 4.2e-20;
Matches 49; Conservative 17; Mismatches 38; Indels 14; Gaps 5;

OY 3 GLDCDEHSTESRCRCRYPLTVDFEAFGW-DWIAPKRYKANYCSGCEGFVFLQKYP----- 56
DB 277 GLECDGRT--NLCCRQGFYIDFRLIGMNDWIAPSGYGNCEGSCP-AYLAGVPSASS 333
OY 57 -HTHLVHQANPR---GSAGPCCPTKSPINMLYFNGEGQIYIGKIPAMVVDRCGS 109
DB 334 FHTAVVQYRMRLNPGVNSCCIPFKLSMSMLYFDDEYNIVKRDVPMNIVEECGCA 391

Search completed: January 31, 2003, 18:21:31
Job time : 8.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 14 Seconds

(without alignments)
748.475 Million cell updates/sec

Title: US-09-620-586b-12

Perfect score: 630

Sequence: 1 DFGIDCDHEHSTESRCCRYPL.....EGQIYGIKIPAMVVDRCGS 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257	40.8	370	2	activin beta B sub
2	251	39.8	255	2	inhibin beta-B cha
3	251	39.8	411	2	inhibin beta-B cha
4	247.5	39.3	115	2	activin beta-B-2 c
5	245	38.9	349	1	inhibin beta-B cha
6	245	38.9	407	1	inhibin beta-B cha
7	245	38.9	408	2	betab inhibin prec
8	244.5	38.8	393	2	activin beta B - z
9	242.5	38.5	115	2	activin beta B-1 c
10	232.5	36.9	207	2	vgr protein - rat
11	232.5	36.9	513	1	bone morphogenetic
12	230.5	36.6	510	2	Vg-1-related prote
13	220	34.9	373	2	activin - fruit fl
14	219	34.8	350	2	transforming growt
15	218.5	34.7	125	2	bone morphogenetic
16	218.5	34.7	436	2	cartilage-derived
17	216.5	34.4	352	2	activin beta C - m
18	216.5	34.4	352	2	activin beta C pre
19	216.5	34.4	360	2	Vgl embryonic grow
20	216.5	34.4	367	2	activin beta D cha
21	215.5	34.2	313	2	bone morphogenetic
22	214.5	34.0	426	2	bone morphogenetic
23	213.5	33.9	413	2	activin beta-A cha
24	213.5	33.9	424	1	inhibin beta-A cha
25	213.5	33.9	424	1	inhibin beta-A cha
26	213.5	33.9	424	1	inhibin beta-A cha
27	213.5	33.9	425	1	inhibin beta-A cha
28	213.5	33.9	425	2	inhibin beta-A cha
29	213.5	33.9	426	1	inhibin beta-A cha

30	212.5	33.7	350	2	JC5241	activin beta E cha
31	212.5	33.7	402	2	A45056	osteogenic protein
32	212.5	33.7	431	1	BMH7	bone morphogenetic
33	211.5	33.6	151	2	S43296	bone morphogenetic
34	211.5	33.6	352	2	JC2466	inhibin beta-C cha
35	210.5	33.4	430	2	J01184	osteogenic protein
36	210.5	33.4	495	2	S43294	bone morphogenetic
37	210.5	33.4	501	2	A55452	cartilage-derived
38	210.5	33.4	501	2	JC2347	growth/differentia
39	208	33.0	366	2	A46607	bone morphogenetic
40	206.5	32.8	452	2	I49542	bone morphogenetic
41	206.5	32.8	454	1	BMH5	bone morphogenetic
42	206	32.7	366	2	A45402	transforming growt
43	203.5	32.3	461	2	S52408	SPDVR1 protein - s
44	201.5	32.0	409	2	S01825	transforming growt
45	201.5	32.0	410	2	A41397	transforming growt

ALIGNMENTS

RESULT 1

activin beta B subunit - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
R:Dohrmann, C.E.; Hemmati-Brianlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melton, Dev. Biol. 157, 474-483, 1993
A>Title: Expression of activin mRNA during early development in Xenopus laevis.
A:Reference number: 151199; MUID:93273083; PMID:8500654
A:Accession: 151199
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-370 <DOH>
A:Cross-references: GB:S61773; NID:9386027; PIDN:AAB26863.1; PID:9386028
C:Superfamily: inhibin

Query Match 40.8%; Score 257; DB 2; Length 370;
Best Local Similarity 43.2%; Pred. No. 5.8e-20;
Matches 51; Conservative 16; Mismatches 37; Indels 14; Gaps 5;

QY 3 GLDCDEHSTESRCCRYPLTVDPBAFGW-DWIIAPKRYKANYCSGEGEFVFLQKYP----- 56
DB 256 GLECDGHT--NLCCRQGYRIDFRLIGNWDWIIAPAGYGYGNYCEGSCP-AYLAVGSGASS 312
QY 57 -HTHLVHOANPR---GSAGPCCTPTKNSPINMLYFNGEGQIYGIKIPAMVVDRCGS 109
DB 313 FHTAVNQYRMKGLNPGTVNSSCIPFKLSTMSMLYFDDEYNIVKRDVPMIVDECGCA 370

RESULT 2

inhibin beta-B chain - mouse (fragment)
N:Alternate names: activin bb chain
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C:Accession: I48235; I48266; S31441
R:Ritvos, O.; Tuuri, T.; Eramaa, M.; Sainio, K.; Hilden, K.; Saxen, L.; Gilbert, S.F. Mech. Dev. 50, 229-245, 1995
A>Title: Activin disrupts epithelial branching morphogenesis in developing glandular org
A:Reference number: I48235; MUID:95344997; PMID:7619733
A:Accession: I48235
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-234 <RBS>
A:Cross-references: EMBL:X83376; NID:9603571; PIDN:CAA58290.1; PID:9603572
R:Albano, R.M.; Groome, N.; Smith, J.C. Development 117, 711-723, 1993
A>Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cells
A:Reference number: I48243; MUID:93321614; PMID:8330535
A:Accession: I48266
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Cross-references: GB:M31668; GB:M31669; NID:G186419; PIDN:AA59451.1; PID:G386827
R:Masou, A.J.; Miall, H.D.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 135, 957-964, 1986
A:Title: Structure of two human ovarian inhibins.
A:Reference number: A90123; MUID:86186863; PMID:3754442
A:Accession: C24248
A:Molecule type: mRNA
A:Residues: 55-407 <MA2>
A:Cross-references: GB:M13437; NID:G186416; PIDN:AA59169.1; PID:G186417
R:Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.
Mol. Endocrinol. 3, 939-948, 1989
A:Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.
A:Reference number: A40156; MUID:89295443; PMID:2739657
A:Accession: A40156
A:Molecule type: mRNA
A:Residues: 22-46, 'A', 48-407 <FEN>
A:Cross-references: GB:M31632
A:Experimental source: testis
R:Schmeizler, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, N.
Biochim. Biophys. Acta 1039, 135-141, 1990
A:Title: Purification and characterization of recombinant human activin B.
A:Reference number: S10751; MUID:90304183; PMID:2364091
A:Accession: S10751
A:Molecule type: protein
A:Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>
C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.
C:Genetics:
A:Gene: GDB:INHBB
A:Cross-references: GDB:119347; OMIM:147390
A:Map position: 2cen-2q13
C:Superfamily: inhibin
C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-292/Domain: propeptide #status predicted <PRO>
F:293/Product: inhibin beta-B chain #status predicted <MAT>
F:93/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.9%; Score 245; DB 1; Length 407;
Best Local Similarity 41.5%; Pred. No. 1.2e-18;
Matches 49; Conservative 17; Mismatches 38; Indels 14; Gaps 5;

QY 3 GLDCDEHSTESRCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCEFFVLOKYP----- 56
Db 293 GLECDGRT--NLCCRQGFIDFRLIGWMDWIIAPTYGYGNYCEGSCP-AYLAGVPGSASS 349

QY 57 -HTHLVHQANPR---GSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
Db 350 FHTAVVNVQYRMKGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPMNIVEECGCA 407

RESULT 7
S50899
betab inhibin precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C:Accession: S50899
R:Thompson, D.A.; Cronin, C.N.; Martin, F.
Eur. J. Biochem. 226, 751-764, 1994
A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and beta(B)
Y DNase I footprinting.
A:Reference number: S50897; MUID:95112839; PMID:7813465
A:Accession: S50899
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-408 <THO>
A:Cross-references: EMBL:U16240
C:Genetics:
A:Introns: 151/1
C:Superfamily: inhibin

Query Match 38.9%; Score 245; DB 2; Length 408;
Best Local Similarity 41.5%; Pred. No. 1.2e-18;

Matches 49; Conservative 17; Mismatches 38; Indels 14; Gaps 5;

QY 3 GLDCDEHSTESRCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCEFFVLOKYP----- 56
Db 294 GLECDGRT--NLCCRQGFIDFRLIGWMDWIIAPTYGYGNYCEGSCP-AYLAGVPGSASS 350

QY 57 -HTHLVHQANPR---GSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
Db 351 FHTAVVNVQYRMKGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPMNIVEECGCA 408

RESULT 8
I50103
activin beta B - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: I50103
R:Witbrodt, J.; Rosa, F.M.
Genes Dev. 8, 1448-1462, 1994
A:Title: Disruption of mesoderm and axis formation in fish by ectopic expression of acti
A:Reference number: I50103; MUID:95011555; PMID:7926744
A:Accession: I50103
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-393 <WIT>
A:Cross-references: EMBL:X76051; NID:G516356; PIDN:CA53636.1; PID:G516357
C:Genetics:
A:Gene: Zactbetab
C:Superfamily: inhibin

Query Match 38.8%; Score 244.5; DB 2; Length 393;
Best Local Similarity 41.5%; Pred. No. 1.4e-18;
Matches 49; Conservative 17; Mismatches 39; Indels 13; Gaps 5;

QY 3 GLDCDEHSTESRCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCEFFVLOKYP----- 56
Db 278 GLECDGNN-GGLCCRQGFIDFRLIGWMDWIIAPAGYGNICEGSCP-AYMAGVPGSASS 335

QY 57 -HTHLVHQANPR---GSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
Db 336 FHTAVVNVQYRMKGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPMNIVEECGCA 393

RESULT 9
PN0505
activin beta B-1 chain - goldfish (fragment)
N:Alternate names: gact 2
C:Species: Carassius auratus (goldfish)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PN0505
R:Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.
Biochem. Biophys. Res. Commun. 193, 711-717, 1993
A:Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural con
A:Reference number: PN0504; MUID:93290666; PMID:8512569
A:Accession: PN0505
A:Molecule type: DNA
A:Residues: 1-115 <GEW>
C:Superfamily: inhibin

Query Match 38.5%; Score 242.5; DB 2; Length 115;
Best Local Similarity 41.9%; Pred. No. 6.3e-19;
Matches 49; Conservative 15; Mismatches 40; Indels 13; Gaps 5;

QY 3 GLDCDEHSTESRCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCEFFVLOKYP----- 56
Db 1 GLECD-GTNGGLCCRQGFYIDFRLIGWMDWIIAPAGYGNICEGSCP-AYMAGVPGSASS 58

QY 57 -HTHLVHQANPR---GSAGPCCPTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGC 108
Db 59 FHTAVVNVQYRMKGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPMNIVEECGC 115

RESULT 10

S37618
vgr protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Feb-1994 #sequence_revision 26-May-1995 #text_change 16-Jul-1999
C:Accession: S37618
R:Sauermann, U.; Meyermann, R.; Schluesener, H.J.
J. Neurosci. Res. 33, 142-147, 1992
A:Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brain: cloning
A:Reference number: S37618; MUID:93085758; PMID:1453478
A:Accession: S37618
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-207 <SAU>
A:Cross-references: EMBL:X58830; NID:G57475; PIDN:CAA41634.1; PID:G57476
A:Note: the sequences from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser
C:Superfamily: inhibin

Query Match	36.9%;	Score 232.5;	DB 2;	Length 207;
Best Local Similarity	42.3%;	Pred. No. 1.4e-17;		
Matches 47;	Conservative 13;	Mismatches 44;	Indels 7;	Gaps 2;

```
QY      5 DCDENHSTESRCRYPLTVDEAFGW-DWIIAPKRRYKANVCSGCECFEVLÖKYPTH----- 59
          |::|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::|:
Db     96 DYNSELKTACKRHIELYVSFDLLGWQDWTIAPKGYAANYCDEGCSEFLNAHMMAATNHAIIV 155
```

```
Qy 60 --LVHGANPRGSAGPCCCTPTKMSPINMLTFNGEGQIIYGIKIPAMVVDRCGC 108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 156 QTLVHLMNPEYVVPKPCCAPTKLNATSVLYEDDNSVILKKYRNMVVRACGC 206
```

RESULT 11

bone morphogenetic protein 6 precursor - human

```
C:\Species: Homo sapiens (man)
C:\Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:\Accession: B39263
```

R:Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Woelz, Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
A:Title: Identification of transforming growth factor beta family members present in bono
A:Reference number: A39263; MUID:91088608; PMID:2263636

A:Accession: B39263
A:Molecule type: mRNA
A:Residues: 1-513 <CEL>
A:Cross-references: GB:M60315; GB:M38664; NID:g339561; PIDN:AAA36737.1; PID:g3395622

A;Gene: GDB:BMP6
A;Cross-references: GDB:127596; OMIM:112266
A;Map position: 6pter-6qter

C:Keywords: bone; glycoprotein
F.1-23/Domain: signal sequence #status predicted <SIG>
F.24-374/Domain: propeptide #status predicted <PRO>
F.375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>
F.241, 269, 386, 404, 454/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	36.98;	Score 232.5;	DB 1;	Length 513;
Best Local Similarity	42.38;	Pred. No. 3.5e-17;		
Matches 47;	Conservative 13;	Mismatches 44;	Indels 7;	Gaps 2;

```
QY      5 DCDHEHSTESRCRRPLTVDEAFEGW-DWIIAPKRYKANYCSGECEFEVLQKYPPTH----- 59
      | : : : | : : | | | | | | | | | | | | | | | | :
DB 402 DYNSELKTACRKHELYVSFODLGMQDWIATPKGYAANYCDGECSPFLNAHMMATNHAIV 451
```

QY 60 ~LVHONPRGSAGPCCCTPTKSPINMLTFNGEGQIIYGKIPIAMVVDRCGC 108
 ||| ||| ||| : : : : : : : ||| |||
Db 462 QTLVHLNMPEYVPKPCCAPTKLNATISVLFFDDNSNVIILKKYRNMVVRRACGC 512

RESULT 12

Vg-1-related protein precursor - mouse
 C1Species: Mus musculus (house mouse)
 C1Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999

C;Accession: A54798; A33925; S47442
R;Gitelman, S.E.; Kobrin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Derynck, R.
J. Cell Biol. 126, 1595-1609, 1994
A;Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral bone
A;Reference number: A54798; MUID:94375533; PMID:8089189
A;Accession: A54798
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-510 <GIT>
A;Cross-references: EMBL:X80992; NID:g530729; PIDD:CAA56917.1; PID:g530730
R;Lyons, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.; Hogan, B.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989
A;Title: Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the transforming
A;Reference number: A33925; MUID:89282810; PMID:2734307
A;Accession: A33925
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'M', '74', 'K', '76-85', 'P', '87-510 <LYO>
A;Cross-references: GB:J04566; NID:g202352; PIDD:AAA40548.1; PID:g202353
C;Superfamily: inhibin

Query Match	36.6%;	Score 230.5;	DB 2;	Length 510;
Best Local Similarity	42.3%;	Pred. No. 5.6e-17;		
Matches 47;	Conservative 13;	Mismatches 44;	Indels 7;	Gaps 2;

```

5 DCDSESTESRCCRPPLTVDFEAFGM-DWIIAPKRYKANYCSGECEFEVLQKYPTH----- 59
   | : :: ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
399 DYNGSELTKACKKHGLYVSFDQLGWODWTIAPKGYANVCDEGCSPPLNAHMAATNHAIIV 458
```

```
QY      60 --LVHQANPFGSAGPCCTFTKSPINMLYFNGEGQIIYGKI PAMVVDRCGC 108
        ||| || | ||| ||| : ||| ||| : ||| ||| |||
Db      459 QTLVLHLMPEVVPKPCCAPTKINALSLVIFYDDNSNVILIKIRNMYVRACGC 509
```

RESULT 13

activin - fruit fly (*Drosophila* sp.) (fragment)

C:Species: *Drosophila* sp.
C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Nov-2000
C:Accession: PM0042
R:Kutty, G.; Kutty, R.K.; Samuel, W.; Duncan, T.; Jaworski, C.; Wiggert, B.

Biochem. Biophys. Res. Commun. 246, 644-649, 1998
A>Title: Identification of a new member of transforming growth factor-beta superfamily
A;Reference number: PM0042; MUID:98289585; PMID:9618266
A;Accession: PM0042

A;Molecule type: mRNA
A;Residues: 1-373 <KUT>
A;Cross-references: GB:AF054822
C;Genetics:

A;Cross-references: FlyBase:FBgn0024913
A;Start codon: GGT
A;Introns: 86/3
C;Superfamily: inhibin

Query Match	34.9%;	Score 220;	DB 2;	Length 373;
Best Local Similarity	39.5%;	Pred. No. 5.5e-16;		
Matches 45;	Conservative 17;	Mismatches 40;	Indels 12;	Gaps 6;

```
QY      4 LDDDEHSTESRCRRPLTWDFEAFGM-DWIIAPKRYKANYCSGECEVF-----LQKYPH 57
       :|:   :||: |:||| |||||:| |||||:| |:|
Db      262 VDCG-GALNGCCCKESFYYSFKALGWMDWIAPRGTFANYCRGDGTGSFRTPTDQTGF-H 319
```

Qy 58 THLVHQANPRG--SAGPCCTPTPKNSPIMLTLYENGEGQIIYGIKIPAMVVDRCGC 108
| : : | | | : : : : : | : | | | | |
Db 320 AHFIEERYKMGMLNMGMRPCCAPLEFSSMSLTYGDG-IIKRDLPKMVDVDECGC 372

RESULT 14

transforming growth factor beta homolog - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C/Accession: T23451

10

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 14 Seconds

(without alignments)
748.475 Million cell updates/sec

Title: US-09-620-586B-11

Perfect score: 629

Sequence: 1 DFGLDCEHSTESRCCRYPL.....KEQIYGIKIPAMVVDRCGS 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	254	40.4	370	2 151199	activin beta B sub
2	248	39.4	255	2 148235	inhibin beta-B cna
3	248	39.4	411	2 B41398	inhibin beta-B cna
4	244.5	38.9	115	2 PN0506	activin beta B-2 c
5	242	38.5	349	1 WFPGBB	inhibin beta-B cna
6	242	38.5	407	1 A40150	inhibin beta-B cna
7	242	38.5	408	2 S50899	betab inhibin prec
8	241.5	38.4	393	2 I50103	activin beta B - 2
9	239.5	38.1	115	2 PN0505	activin beta B-1 c
10	232.5	37.0	207	2 S37618	vgr protein - rat
11	232.5	37.0	513	1 BMH06	bone morphogenetic
12	230.5	36.6	510	2 A54798	Vg-1-related prote
13	219.5	34.9	360	2 A29619	Vg1 embryonic grow
14	218.5	34.7	125	2 S43295	bone morphogenetic
15	218.5	34.7	436	2 B55452	cartilage-derived
16	218	34.7	373	2 PM0042	activin - fruit fl
17	217.5	34.6	413	2 JC4862	inhibin beta-A cha
18	217.5	34.6	424	1 WFPGBA	inhibin beta-A cha
19	217.5	34.6	424	1 S31440	inhibin beta-A cha
20	217.5	34.6	424	1 B40905	inhibin beta-A cha
21	217.5	34.6	425	1 S50898	inhibin beta-A cha
22	217.5	34.6	425	1 I47072	inhibin beta-A cha
23	217.5	34.6	426	1 B24248	inhibin beta-A cha
24	216.5	34.4	367	2 JC4151	activin beta D cha
25	215.5	34.3	313	2 I51284	bone morphogenetic
26	213.5	33.9	352	2 JC5366	activin beta C - m
27	213.5	33.9	352	2 S70580	activin beta C pre
28	213.5	33.9	426	2 JH0690	bone morphogenetic
29	212.5	33.8	402	2 A45056	osteogenic protein

30	212.5	33.8	431	1 BMH07	bone morphogenetic
31	211.5	33.6	151	2 S43296	bone morphogenetic
32	210.5	33.5	430	2 JQ1184	osteogenic protein
33	210.5	33.5	495	2 S43294	bone morphogenetic
34	210.5	33.5	501	2 A55452	cartilage-derived
35	210.5	33.5	501	2 JC2347	growth/differentia
36	208.5	33.1	352	2 JC2466	inhibin beta-C cha
37	208	33.1	350	2 T25451	transforming growt
38	208	33.1	366	2 A46607	growth/differentia
39	208	33.1	393	2 S37073	bone morphogenetic
40	208	33.1	394	2 S45355	bone morphogenetic
41	208	33.1	396	1 BMH02	bone morphogenetic
42	208	33.1	398	2 JH0688	bone morphogenetic
43	208	33.1	398	2 JH0687	bone morphogenetic
44	207	32.9	353	2 I50607	bone morphogenetic
45	206.5	32.8	452	2 I49542	bone morphogenetic

ALIGNMENTS

RESULT 1

activin beta B subunit - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999

C/Accession: I51199

R.Dohrmann, C.E.; Hemmati-Britvanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melton, Dev. Biol. 157, 474-483, 1993

A/Title: Expression of activin mRNA during early development in Xenopus laevis.

A/Reference number: I51199; MUID:93273083; PMID:8500654

A/Accession: I51199

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-370 <DOH>

A/Cross-references: GB:S61773; NID:G386027; PIDN:AA26863.1; PID:G386028

C/Superfamily: Inhibin

Query Match

Best Local Similarity 40.4%; Score 254; DB 2; Length 370;
Matches 50; Conservative 17; Mismatches 37; Indels 14; Gaps 5;

QY 3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCEFEVFLQKVP----- 56
DB 256 GLECDGHT--NLCCRQGFYIDFRLIGWMDWIIAPAGYGNVCEGSCP-AVLAVPGSASS 312
QY 57 -HTHLVHOANPR---GSAGPCCTPTKMSPINMLYFNKKEQIYGIKIPAMVVDRCGS 109
DB 313 FHTAVVNQYMRGLNPGTVNSCIPTKLSTMSMLYFDDEYNIWKRDVPMIVDECGCA 370

RESULT 2

I48235 inhibin beta-B chain - mouse (fragment)

N/Alternate names: activin hb chain

C/Species: Mus musculus (house mouse)

C/Date: 02-Jul-1996 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999

C/Accession: I48235; I48266; S31441

R.Ritvos, O.; Tuuri, T.; Eramaa, M.; Sainio, K.; Hilden, K.; Saxen, L.; Gilbert, S.F. Mech. Dev. 50, 229-245, 1995

A/Title: Activin disrupts epithelial branching morphogenesis in developing glandular org

A/Reference number: I48235; MUID:95344997; PMID:7619733

A/Accession: I48235

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-234 <REB>

A/Cross-references: EMBL:X83376; NID:G603571; PIDN:CAA58290.1; PID:G603572

R.Albano, R.M.; Groom, N.; Smith, J.C. Development 117, 711-723, 1993

A/Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cells

A/Reference number: I48243; MUID:93321614; PMID:8330535

A/Accession: I48266

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; PID:g386827
R/Mason, A.J.; Niall, H.D.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 135, 957-964, 1986
A/Title: Structure of two human ovarian inhibins.
A/Reference number: A90123; MUID:86186863; PMID:3754442
A/Accession: C24248
A/Molecule type: mRNA
A/Residues: 55-407 <MA2>
A/Cross-references: GB:M13437; NID:g186416; PIDN:AAA59169.1; PID:g186417
R/Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.
Mol. Endocrinol. 3, 939-948, 1989
A/Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.
A/Reference number: A40156; MUID:89295443; PMID:2739657
A/Accession: A40156
A/Molecule type: mRNA
A/Residues: 22-46, 'A', 48-407 <FEN>
A/Cross-references: GB:M31632
A/Experimental source: testis
R/Schmeizler, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, N.
Biochim. Biophys. Acta 1039, 135-141, 1990
A/Title: Purification and characterization of recombinant human activin B.
A/Reference number: S10751; MUID:90304183; PMID:2364091
A/Accession: S10751
A/Molecule type: protein
A/Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>
C/Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.
bin beta-A and beta-B, respectively.
C/Genetics:
A/Gene: GDB:INHB
A/Cross-references: GDB:119347; OMIM:147390
A/Map position: 2cen-2q13
C/Superfamily: inhibin
C/Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-292/Domain: propeptide #status predicted <PRO>
F/293/Product: inhibin beta-B chain #status predicted <MAT>
F/93/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 38.5%; Score 242; DB 1; Length 407;
Best Local Similarity 40.7%; Pred. No. 1.8e-18;
Matches 48; Conservative 18; Mismatches 38; Indels 14; Gaps 5;

QY 3 GLDCDEHSTESRCRYPPLTVDFEAFGW-DWIIAPKRYKANYCSGECEVFLOKYP----- 56
Db 293 GLECDGRT--NLCCRQGFIDFRLIGMNDWIIAPGTGYGNYCEGSCP-AYLAGVPGSASS 349

QY 57 -HTHLVHQANPR---GSAGPCCPTPTKMSPINMLYFNKGEOIITYGKIPAMVVDRCGCS 109
Db 350 FHTAVVNQYRMGRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 407

RESULT 7
S50899
betab inhibin precursor - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C/Accession: S50899
R/Thompson, D.A.; Cronin, C.N.; Martin, F.
Eur. J. Biochem. 226, 751-764, 1994
A/Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and beta(B)
Y DNase I footprinting.
A/Reference number: S50897; MUID:95112839; PMID:7813465
A/Accession: S50899
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-408 <THO>
A/Cross-references: EMBL:U16240
C/Genetics:
A/Introns: 151/1
C/Superfamily: inhibin

Query Match 38.5%; Score 242; DB 2; Length 408;
Best Local Similarity 40.7%; Pred. No. 1.8e-18;

Matches 48; Conservative 18; Mismatches 38; Indels 14; Gaps 5;

QY 3 GLDCDEHSTESRCRYPPLTVDFEAFGW-DWIIAPKRYKANYCSGECEVFLOKYP----- 56
Db 294 GLECDGRT--NLCCRQGFIDFRLIGMNDWIIAPGTGYGNYCEGSCP-AYLAGVPGSASS 350

QY 57 -HTHLVHQANPR---GSAGPCCPTPTKMSPINMLYFNKGEOIITYGKIPAMVVDRCGCS 109
Db 351 FHTAVVNQYRMGRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 408

RESULT 8
I50103
activin beta B - zebra fish
C/Species: Brachydanio rerio (zebra fish)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C/Accession: I50103
R/Wittbrodt, U.; Rosa, F.M.
Genes Dev. 8, 1448-1462, 1994
A/Title: Disruption of mesoderm and axis formation in fish by ectopic expression of acti
A/Reference number: I50103; MUID:95011555; PMID:7926744
A/Accession: I50103
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-393 <WIT>
A/Cross-references: EMBL:X76051; NID:g516356; PIDN:CAA53636.1; PID:g516357
C/Genetics:
A/Gene: Zactbetab
C/Superfamily: inhibin

Query Match 38.4%; Score 241.5; DB 2; Length 393;
Best Local Similarity 40.7%; Pred. No. 1.9e-18;
Matches 48; Conservative 18; Mismatches 39; Indels 13; Gaps 5;

QY 3 GLDCDEHSTESRCRYPPLTVDFEAFGW-DWIIAPKRYKANYCSGECEVFLOKYP----- 56
Db 278 GLECDGNN-GGLCCRQGFYIDFRLIGMNDWIIAPAGYGYGNYCEGSCP-AYMAGVPGSASS 335

QY 57 -HTHLVHQANPR---GSAGPCCPTPTKMSPINMLYFNKGEOIITYGKIPAMVVDRCGCS 109
Db 336 FHTAVVNQYRMGRGSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 393

RESULT 9
PN0505
activin beta B-1 chain - goldfish (fragment)
N/Alternate names: gact 2
C/Species: Carassius auratus (goldfish)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C/Accession: PN0505
R/Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.
Biochem. Biophys. Res. Commun. 193, 711-717, 1993
A/Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural con
A/Reference number: PN0504; MUID:93290666; PMID:8512569
A/Accession: PN0505
A/Molecule type: DNA
A/Residues: 1-115 <GEW>
C/Superfamily: inhibin

Query Match 38.1%; Score 239.5; DB 2; Length 115;
Best Local Similarity 41.0%; Pred. No. 9.1e-19;
Matches 48; Conservative 16; Mismatches 40; Indels 13; Gaps 5;

QY 3 GLDCDEHSTESRCRYPPLTVDFEAFGW-DWIIAPKRYKANYCSGECEVFLOKYP----- 56
Db 1 GLECD-GTNGGLCCRQGFYIDFRLIGMNDWIIAPAGYGYGNYCEGSCP-AYMAGVPGSASS 58

QY 57 -HTHLVHQANPR---GSAGPCCPTPTKMSPINMLYFNKGEOIITYGKIPAMVVDRCGC 108
Db 59 FHTAVVNQYRMGRGISPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGC 115

RESULT 10

A>Title: Lfmb alterations in brachypodism mice due to mutations in a new member of the T

A/Reference number: S43294; MUID:94195427; PMID:8145850

A/Accession: S43295

A/Molecule type: DNA

A/Residues: 1-125 <STO>

A/Cross-references: EMBL:U08338; NID:G488463; PIDN:AAA18779.1; PID:G488464

C/Genetics:

A/Gene: Gdf6

C/Superfamily: inhibin

F/1-5/Domain: polybasic protease recognition site #status predicted <PR>

F/6-125/Product: bone morphogenetic protein homolog GDF6 (fragment) #status predicted <M

Query Match

Best Local Similarity 34.7%; Score 218.5; DB 2; Length 125;

Matches 43; Conservative 19; Mismatches 38; Indels 9; Gaps 4;

QY

9 HSTES--RCRRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCEFFVFLQKY-PHTH----- 59

16 HGKKSRLRCGRKPLHVNFKELGMDWIIAPLEYEAYHCEGVCDPRLRSHLEPTNHAIIQT 75

QY

60 LVHQANPRGSAGPCCTPTKSPINMLYFNGKEQIIYGKIPAMVVDRCGC 108

76 LMNSMDPGSTPPSCCVPTKLTPIISILYIDAGNNVVYKQYEDMVVESCGC 124

RESULT 15

B55452

cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000

C/Accession: B55452

R/Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak

J. Biol. Chem. 269, 28227-28234, 1994

A>Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth

A/Reference number: A55452; MUID:95050604; PMID:7961761

A/Accession: B55452

A/status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-436 <CHA>

A/Cross-references: GB:U13661; NID:G632489; PIDN:AAA61416.1; PID:G632490

C/Superfamily: inhibin

Query Match

Best Local Similarity 34.7%; Score 218.5; DB 2; Length 436;

Matches 42; Conservative 20; Mismatches 38; Indels 9; Gaps 4;

QY

9 HSTES--RCRRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCEFFVFLQKY-PHTH----- 59

16 HGKKSRLRCGRKPLHVNFKELGMDWIIAPLEYEAYHCEGVCDPRLRSHLEPTNHAIIQT 75

QY

60 LVHQANPRGSAGPCCTPTKSPINMLYFNGKEQIIYGKIPAMVVDRCGC 108

76 LMNSMDPGSTPPSCCVPTKLTPIISILYIDAGNNVVYKQYEDMVVESCGC 124

Search completed: January 31, 2003, 18:18:58
Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 8.5 Seconds

(without alignments)
531.873 Million cell updates/sec

Title: US-09-620-586B-11

Perfect score: 629
Sequence: 1 DFGLDCEHSTESRCCRYPL.....KEQIYGIKIPAMVDRCGCS 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	629	100.0	375	1	GDF8_CHICK
2	629	100.0	375	1	GDF8_HUMAN
3	629	100.0	375	1	GDF8_MELGA
4	629	100.0	375	1	GDF8_PIG
5	629	100.0	375	1	GDF8_MOUSE
6	629	100.0	375	1	GDF8_MOUSE
7	623	99.0	375	1	GDF8_MOUSE
8	619	98.4	375	1	GDF8_PAPHA
9	618	98.3	375	1	GDF8_SHEEP
10	581	92.4	405	1	GDF8_BOVIN
11	581	92.4	405	1	GDF8_MOUSE
12	570	90.6	374	1	GDF8_HUMAN
13	534	84.9	345	1	GDF8_RAT
14	248	39.4	255	1	IHBB_MOUSE
15	246	39.1	355	1	DVRL_BRARE
16	243	38.6	391	1	IHBB_CHICK
17	242	38.5	407	1	IHBB_PIG
18	242	38.5	407	1	IHBB_HUMAN
19	242	38.5	408	1	IHBB_BOVIN
20	232.5	37.0	207	1	BMP6_RAT
21	232.5	37.0	513	1	BMP6_HUMAN
22	230.5	36.6	510	1	BMP6_MOUSE
23	223.5	35.5	426	1	IHBA_HORSE
24	219.5	34.9	360	1	DVRL_XENLA
25	218.5	34.7	125	1	GDF6_MOUSE
26	218.5	34.7	436	1	GDF6_BOVIN
27	217.5	34.6	424	1	IHBA_MOUSE
28	217.5	34.6	424	1	IHBA_PIG
29	217.5	34.6	424	1	IHBA_RAT
30	217.5	34.6	425	1	IHBA_BOVIN
31	217.5	34.6	425	1	IHBA_SHEEP
32	217.5	34.6	425	1	IHBA_HUMAN
33	213.5	33.9	352	1	IHBC_MOUSE

34	213.5	33.9	426	1	BMP7_XENLA	P30886 xenopus lae
35	212.5	33.8	402	1	BMP8_HUMAN	P34820 homo sapien
36	212.5	33.8	431	1	BMP7_HUMAN	P18075 homo sapien
37	211.5	33.6	151	1	GDF7_MOUSE	P43029 mus musculu
38	210.5	33.5	430	1	BMP7_MOUSE	P23359 mus musculu
39	210.5	33.5	495	1	GDF5_MOUSE	P43027 mus musculu
40	210.5	33.5	501	1	GDF5_HUMAN	P43026 homo sapien
41	208.5	33.1	352	1	IHBC_HUMAN	P55103 homo sapien
42	208.5	33.1	395	1	UNIV_STRPU	P48970 strongyloce
43	208.5	33.1	424	1	IHBA_CHICK	P27092 gallus gall
44	208	33.1	350	1	DAF7_CAEEL	P21172 caenorhabdi
45	208	33.1	366	1	GDF3_MOUSE	Q07104 mus musculu

ALIGNMENTS

RESULT 1	ID	GDF8_CHICK	STANDARD;	PRT;	375 AA.
AC	O42220	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, last sequence update)				
DT	16-OCT-2001 (Rel. 40, last annotation update)				
DE	Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).				
GN	GDF8 OR MSTN.				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=white leghorn; TISSUE=skeletal muscle;				
RX	MEDLINE=98024153; PubMed=9356471;				
RA	McPherron A.C., Lee S.-J.;				
RT	"Double muscling in cattle due to mutations in the myostatin gene.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).				
CC	-!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL MUSCLE GROWTH.				
CC	-!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).				
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.				
CC	-----				
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CC	-----				
DR	EMBL; AF019621; AAB86688.1; -				
DR	HSSP; P18075; 1BMP.				
DR	InterPro; IPR001839; TGFb.				
DR	InterPro; IPR001111; TGFb N.				
DR	Pfam; PF00019; TGF-beta; 1.				
DR	Pfam; PF00688; TGFb propeptide; 1.				
DR	ProDom; PD000357; TGFb; 1.				
DR	SMART; SM00204; TGFb; 1.				
DR	PROSITE; PS00250; TGF_BETA_1; 1.				
KW	Growth factor; Cytokine; Glycoprotein; Signal.				
FT	SIGNAL	1	23		POTENTIAL.
FT	PROPEP	24	266		POTENTIAL.
FT	CHAIN	267	375		GROWTH/DIFFERENTIATION FACTOR 8.
FT	DISULFID	281	340		BY SIMILARITY.
FT	DISULFID	309	372		BY SIMILARITY.
FT	DISULFID	313	374		BY SIMILARITY.
FT	DISULFID	339	339		INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD	71	71		N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	375 AA;	42707 MW;		DA732DB9426E4DAF CRC64;

Query Match 100.0%; Score 629; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.2e-62;


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Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVLQKYPHTL 60
   |||
Db 267 DFGLDDEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVLQKYPHTL 326

QY 61 VHOANRGSAGPCCPTPTXMSPINMLYFNKGEOIIVYKIPAMVVDRCGS 109
   |||
Db 327 VHOANRGSAGPCCPTPTXMSPINMLYFNKGEOIIVYKIPAMVVDRCGS 375

RESULT 2
GDF8_HUMAN
ID_GDF8_HUMAN STANDARD; PRT; 375 AA.
AC 014793;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=99061972; PubMed=9843994;
RA Gonzalez-Cadavid N.F., Taylor W.E., Yarasheski K., Sinha-Hikim I.,
RA Ma K., Ezzat S., Shen R., Lalani R., Asa S., Mamita M., Nair G.,
RA Arver S., Bhasin S.;
RT "Organization of the human myostatin gene and expression in healthy
RT men and HIV-infected men with muscle wasting.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14938-14943 (1998).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF019627; AAB86694.1; -.
DR EMBL; AF104922; AAC96327.1; -.
DR HSSP; P18075; IBMP.
DR Genew; HGNC:4223; GDF8.
DR MIM; 601788; -.
DR InterPro; IPR001839; TGFb_N.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta_1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 266 POTENTIAL.
FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 281 340 BY SIMILARITY.
FT DISULFID 309 372 BY SIMILARITY.
FT DISULFID 313 374 BY SIMILARITY.

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FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 375 AA; 42750 MW; B8F66129725E6AFA CRC64;

Query Match
Best Local Similarity 100.0%; Score 629; DB 1; Length 375;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEGLDCDEHSTERRCRCRYPLTYDFFAFGWDWITAPKRYKANCSCGECEVFVLOKYPHTHL 60
   |||||||
Db 267 DEGLDCDEHSTERRCRCRYPLTYDFFAFGWDWITAPKRYKANCSCGECEVFVLOKYPHTHL 326

QY 61 VHOANPRGSAGPCTCTPTKMSPIINMLYFNKGEOITYGKIPAMVVDRCGCS 109
   |||||||
Db 327 VHOANPRGSAGPCTCTPTKMSPIINMLYFNKGEOITYGKIPAMVVDRCGCS 375

RESULT 3
GDF8_MELGA STANDARD; PRT; 375 AA.
ID GDF8_MELGA
AC 042221;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OK NCBI_TaxID=9103;
RN 11)
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-----
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-----
CC EMBL; AF019625; AAB86692.1; ALT_INIT.
DR HSSP; P18075; IBMF.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KM Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 266 POTENTIAL.
FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 281 340 BY SIMILARITY.
FT DISULFID 309 372 BY SIMILARITY.
FT DISULFID 313 374 BY SIMILARITY.
FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 375 AA; 42784 MW; D2AEAB732AEB4E77 CRC64;

Query Match
Best Local Similarity 100.0%; Score 629; DB 1; Length 375;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DFGLDCEHSTSRCCRYPLTVDFEAFGMDWITAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGLDCEHSTSRCCRYPLTVDFEAFGMDWITAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNKGQIYKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNKGQIYKIPAMVVDRCGCS 375

RESULT 4
GDF8_PIG STANDARD; PRT; 375 AA.
ID GDF8_PIG STANDARD; PRT; 375 AA.
AC 018831;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Duroc, Hampshire, Meishan, and Yorkshire;
RC TISSUE=Skeletal muscle;
RA Voelker G.R., Conroy J.C., Wheeler M.B.;
RT "Porcine myostatin cDNA sequences: Duroc, Hampshire, Meishan and
Yorkshire pigs";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-10 AND 36-375 FROM N.A.
RC TISSUE=Muscle;
RA Daneau I., Silversides D.W.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
CC EMBL; AF019623; AAB86690.1; -
DR EMBL; AF188635; AAF02770.1; -
DR EMBL; AF188636; AAF02771.1; -
DR EMBL; AF188637; AAF02772.1; -
DR EMBL; AF188638; AAF02773.1; -
DR EMBL; AF033855; AAC08035.1; -
DR EMBL; AF093798; AAC62489.1; -
DR HSSP; P18075; IBMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SMO0204; TGFb; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SMO0204; TGFb; 1.
DR Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.

FT PROPEP 24 266 POTENTIAL.
FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 281 340 BY SIMILARITY.
FT DISULFID 309 372 BY SIMILARITY.
FT DISULFID 313 374 BY SIMILARITY.
FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 71 71 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 375 AA; 42791 MW; 0F658685EFD43418 CRC64;

Query Match 100.0%; Score 629; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.2e-62;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTSRCCRYPLTVDFEAFGMDWITAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGLDCEHSTSRCCRYPLTVDFEAFGMDWITAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNKGQIYKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNKGQIYKIPAMVVDRCGCS 375

RESULT 5
GDF8_MOUSE STANDARD; PRT; 376 AA.
ID GDF8_MOUSE STANDARD; PRT; 376 AA.
AC 008689;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Skeletal muscle;
RX MEDLINE=97284412; PubMed=9139826;
RA McPherron A.C., Lawler A.M., Lee S.-J.;
RT "Regulation of skeletal muscle mass in mice by a new TGF-beta
superfamily member";
RL Nature 387:83-90(1997).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT
SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-COITUM IN
ONE-THIRD OF DEVELOPING SOMITES. AT DAY 10.5, EXPRESSED IN THE
MYOTOME COMPARTMENT OF SOMITES. AT LATER STAGES OF DEVELOPMENT,
DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION
CONTINUES IN ADULTHOOD.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U84005; AAC53167.1; -
DR HSSP; P18075; IBMP.
DR MGD; MG1:95691; Gdf8.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SMO0204; TGFb; 1.
DR ProSite; PS00250; TGF_BETA_1; 1.

KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT PROPEP 25 267 POTENTIAL.
FT CHAIN 268 376 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 282 341 BY SIMILARITY.
FT DISULFID 310 373 BY SIMILARITY.
FT DISULFID 314 375 BY SIMILARITY.
FT CARBOHYD 340 340 INTERCHAIN (BY SIMILARITY).
SQ SEQUENCE 376 AA; 42921 MW; 3E19814DD62C08BE CRC64; (POTENTIAL).
Query Match 100.0%; Score 629; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.2e-62;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGLCDHEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 268 DFGLCDHEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 327
QY 61 VHOANPRGSAGPCCCTPTKMSPINMLYFNKGKQIYKIPAMVVDRCGCS 109
DB 328 VHOANPRGSAGPCCCTPTKMSPINMLYFNKGKQIYKIPAMVVDRCGCS 376
RESULT 6
GDF8_RAT STANDARD; PRT; 376 AA.
ID GDF8_RAT
AC 035312;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; AF019624; AAB86691.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT PROPEP 25 267 POTENTIAL.
FT CHAIN 268 376 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 282 341 BY SIMILARITY.
FT DISULFID 310 373 BY SIMILARITY.
FT DISULFID 314 375 BY SIMILARITY.

FT DISULFID 340 340 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 376 AA; 42829 MW; 933043D8C8C3294B CRC64;
Query Match 100.0%; Score 629; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.2e-62;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGLCDHEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 268 DFGLCDHEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 327
QY 61 VHOANPRGSAGPCCCTPTKMSPINMLYFNKGKQIYKIPAMVVDRCGCS 109
DB 328 VHOANPRGSAGPCCCTPTKMSPINMLYFNKGKQIYKIPAMVVDRCGCS 376
RESULT 7
GDF8_PAPHA STANDARD; PRT; 375 AA.
ID GDF8_PAPHA
AC 018828;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF019619; AAB86686.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 266 POTENTIAL.
FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 281 340 BY SIMILARITY.
FT DISULFID 309 372 BY SIMILARITY.
FT DISULFID 313 374 BY SIMILARITY.
FT DISULFID 339 374 BY SIMILARITY.
FT CARBOHYD 71 71 INTERCHAIN (BY SIMILARITY).
SQ SEQUENCE 375 AA; 42688 MW; 7B49B90ACAB926EA CRC64; (POTENTIAL).
Query Match 99.0%; Score 623; DB 1; Length 375;
Best Local Similarity 99.1%; Pred. No. 5.8e-62;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGLDCEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVLOKYPHTHL 60
DB 267 DFGLDCEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVLOKYPHTHL 326

OY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGKQIITYGKIIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGKQIITYGKIIPAMVVDRCGCS 375

RESULT 8
GDF8_SHEEP STANDARD; PRT; 375 AA.
ID GDF8_SHEEP
AC 018830; 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; AF019622; AAB86689.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SMD0204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 374
FT CARBOHYD 48 48
FT CARBOHYD 71 71
SQ SEQUENCE 375 AA; 42827 MW; 1C36F3833BB11241 CRC64;

Query Match 98.4%; Score 619; DB 1; Length 375;
Best Local Similarity 97.2%; Pred. No. 1.6e-61;
Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGLDCEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVLOKYPHTHL 60
DB 267 DFGLDCEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVLOKYPHTHL 326

OY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGKQIITYGKIIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGKQIITYGKIIPAMVVDRCGCS 375

RESULT 9
GDF8_BOVIN STANDARD; PRT; 375 AA.
ID GDF8_BOVIN
AC 018836; 018829; 095N97;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN OR MH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT MH TYR-313.
RC STRAIN=Friesian; TISSUE=Muscle, and Embryo;
RX MEDLINE=97458167; PubMed=9314496;
RA Kambadur R., Sharma M., Smith T.P.L., Bass J.J.;
RT "Mutations in myostatin (GDF8) in double-muscled Belgian Blue and
RT Piedmontese cattle.";
RL Genome Res. 7:910-916(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS MH LEU-94 AND TYR-313.
RC STRAIN=Holstein; TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21343337; PubMed=11451380;
RA Jeanplong F., Sharma M., Somers W.G., Bass J.J., Kambadur R.;
RT "Genomic organization and neonatal expression of the bovine myostatin
RT gene.";
RL Mol. Cell. Biochem. 220:31-37(2001).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING AND ADULT
CC SKELETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIMB MUSCLES
CC M.SEMIMEMBRANOSUS AND M.BICEPS FEMORIS; LOW LEVELS IN OTHER
CC HINDLIMB MUSCLES.
CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED THROUGHOUT DEVELOPMENT.
CC LOW LEVELS ARE FOUND UP TO DAY 29 EMBRYOS. LEVELS INCREASE FROM
CC DAY 31 UP UNTIL LATE GESTATION.
CC -1- DISEASE: DEFECTS IN GDF8 ARE THE CAUSE OF THE DOUBLE-MUSCLE
CC PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIVE
CC DISEASE FREQUENTLY FOUND IN THE BELGIAN BLUE AND PIEDMONTES
CC CATTLE BREDS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED
CC NUMBER OF MUSCLE FIBERS (HYPERPLASIA), RESULTING IN AN INCREASE IN
CC MUSCLE MASS OF 20-25%.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; AF019761; AAB81508.1; -.
DR EMBL; AF019620; AAB86687.1; -.
DR EMBL; AF320998; AAG48116.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001839; TGFb.

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DR InterPro: IPR001111; TGF-beta N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta propeptide; 1.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-beta 1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal; Disease mutation.
FT SIGNAL 1 18
FT PROPEP 19 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 339
FT CARBOHYD 47 47
FT CARBOHYD 71 71
FT VARIANT 94 94
FT VARIANT 313 313
FT CONFLICT 14 14
SQ SEQUENCE 375 AA; 42551 MW; 84E1AB20650C05F6 CRC64;

Query Match 98.3%; Score 618; DB 1; Length 375;
Best Local Similarity 98.2%; Pred. No. 2.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPITVDFAFGWDMITAPKRYKANYSGEGCEVFLOKYPHTL 60
DB 267 DFGLDCEHSTESRCRYPITVDFAFGWDMITAPKRYKANYSGEGCEVFLOKYPHTL 326

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGKEQIITGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKMSPINMLYFNGKEQIITGKIPAMVVDRCGCS 375

RESULT 10
GDFB_MOUSE STANDARD; PRT; 405 AA.
ID GDFB_MOUSE STANDARD; PRT; 405 AA.
AC 09Z1W4; 09QX55; 09R221;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein
DE 11).
GN GDF11 OR BMP11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99177155; PubMed=10075854;
RA Gerner J.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
RA Rosen V.;
RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail
RT bud is a potent mesoderm inducer in Xenopus embryos.";
RL Dev. Biol. 208:222-232(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Svj;
RX MEDLINE=99318097; PubMed=10391213;
RA McPherron A.C., Lawler A.M., Lee S.-J.;
RT "Regulation of anterior/posterior patterning of the axial skeleton by
RT growth/differentiation factor 11.";
RL Nat. Genet. 22:260-264(1999).
RN [3]
RP SEQUENCE OF 75-405 FROM N.A.
RX MEDLINE=99173787; PubMed=10072786;
RA Nakashima M., Toyono T., Akamine A., Joyner A.;
RT "Expression of growth/differentiation factor 11, a new member of the
RT BMP/TGF-beta superfamily during mouse embryogenesis.";
RL Mech. Dev. 80:185-189(1999).
CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
CC IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
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CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD,
CC INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING
CC TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT
CC DENTAL PULP AND BRAIN.
CC -1- DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED
CC DOMAINS AT 8.5 DAYS POST COITUS (DPC) WHERE IT IS HIGHEST IN THE
CC TAIL BUD. AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB
CC BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED
CC IN TERMINALLY-DIFFERENTIATED ODONTOBLASTS, THE NASAL EPITHELIUM,
CC RETINA AND SPECIFIC REGIONS OF THE BRAIN.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL: AF100906; AAC72853.1; -.
DR EMBL: AF100904; AAC72853.1; JOINED.
DR EMBL: AF100905; AAC72853.1; JOINED.
DR EMBL: AF028337; AAF21633.1; -.
DR EMBL: AF028335; AAF21633.1; JOINED.
DR EMBL: AF028336; AAF21633.1; JOINED.
DR EMBL: AF092734; AAD05267.1; -.
DR HSSP: P18075; 1BMP.
DR MGD: MGI:1338027; Gdf11.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGF-beta N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta propeptide; 1.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-beta 1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 296
FT CHAIN 297 405
FT DOMAIN 29 39
FT DISULFID 311 370
FT DISULFID 339 372
FT DISULFID 343 404
FT DISULFID 369 369
FT CARBOHYD 92 92
FT CONFLICT 75 75
FT CONFLICT 171 171
SQ SEQUENCE 405 AA; 44946 MW; A74E382710A14781 CRC64;

Query Match 92.4%; Score 581; DB 1; Length 405;
Best Local Similarity 89.9%; Pred. No. 2.9e-57;
Matches 98; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPITVDFAFGWDMITAPKRYKANYSGEGCEVFLOKYPHTL 60
DB 297 NLGLDCEHSTESRCRYPITVDFAFGWDMITAPKRYKANYSGEGCEVFLOKYPHTL 356

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNGKEQIITGKIPAMVVDRCGCS 109
DB 357 VHQANPRGSAGPCCPTPTKMSPINMLYFNGKEQIITGKIPAMVVDRCGCS 405

RESULT 11
GDFB_HUMAN STANDARD; PRT; 407 AA.
ID GDFB_HUMAN STANDARD; PRT; 407 AA.
AC 09S390; 09UID1; 09UID2;
DT 16-OCT-2001 (Rel. 40, Created)
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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein
DE 11).
GN GDF11 OR BMP11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_taxid=9606;
OX 11
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=99177155; PubMed=10075854;
RA Gamber L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
RA Rosen V.;
RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail
RT bud is a potent mesoderm inducer in Xenopus embryos.";
RL Dev. Biol. 208:222-232(1999).
RN 12
RN SEQUENCE FROM N.A.
RX MEDLINE=99318097; PubMed=10391213;
RA McPherron A.C., Lawler A.M., Lee S.-J.;
RT "Regulation of anterior/posterior patterning of the axial skeleton by
RT growth/differentiation factor 11.";
RL Nat. Genet. 22:260-264(1999).
CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
CC IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: secreted (Probable).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; AF100907; AAC72852.1; -.
DR EMBL; AF028333; AAF21630.1; -.
DR EMBL; AF028334; AAF21631.1; -.
DR HSSP; P18075; 1BMP.
DR Genew; HGNC:4216; GDF11.
DR MIM; 603936; -.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR Prodom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT PROPEP 25 298 BY SIMILARITY.
FT CHAIN 299 407 GROWTH/DIFFERENTIATION FACTOR 11.
FT DOMAIN 29 41 POLY-ALA.
FT DISULFID 210 215 POLY-GLY.
FT DISULFID 313 372 BY SIMILARITY.
FT DISULFID 341 404 BY SIMILARITY.
FT DISULFID 345 406 BY SIMILARITY.
FT DISULFID 371 371 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 94 94 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 407 AA; 45090 MW; E8FF48E3635BA8 CRC64;

Query Match 92.4%; Score 581; DB 1; Length 407;
Best Local Similarity 89.9%; Pred. No. 3e-57;
Matches 98; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
1 DFGLDSDHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEEFVLOKYPHTL 60
: |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```
Db      299 NUGLDCDEHSSSRCCRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEYEMQXYPHTHL 358
QY      61 VHOANPRGSAGPCCPTPKMSPINMLYENGKEOIIYGKIPAMVVDRCGCS 109
       | | | | | | | | | | | | | | | | : | | | | | | | | | | |
Db      359 VOQANPRGSAGPCCPTPKMSPINMLYENDKKQIITYGKIPGVVVDRCGCS 407

RESULT 12
GDF8_BRARE STANDARD; PRT; 374 AA.
ID _GDF8_BRARE
AC O42222;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherson A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -! FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -! SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AF019626; AAB86693.1; -.
DR HSSP; PI8075; IBMP.
DR ZFIN; ZDB-GENE-990415-165; gdf8.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF00019; TGF-beta; I.
DR Pfam; PF00688; TGFb propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 265 POTENTIAL.
FT CHAIN 266 374 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 280 339 BY SIMILARITY.
FT DISULFID 308 371 BY SIMILARITY.
FT DISULFID 312 373 BY SIMILARITY.
FT DISULFID 338 338 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 374 AA; 42060 MW; 6302BC6C86562576 CRC64;

Query Match 90.6%; Score 570; DB 1; Length 374;
Best Local Similarity 88.1%; Pred. No. 4, Se-56;
Matches 96; Conservative 11; Mismatches 2; Indels 0; Gaps 0
```


Db 326 VNKASPRGTAGPCTPTKMSPIINMLYFNGKEQIYGIKIPSMVVDRCGS 374

RESULT 13

```

ID  GDFB_RAT          STANDARD;          PRT;          345 AA.
AC  Q92217;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Growth/differentiation factor 11 precursor (Bone morphogenetic protein
    11) (Fragment).
GN  GDF11 OR BMP11.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Dental pulp;
RX  MEDLINE=99173787; PubMed=10072786;
RA  Nakashima M., Toyono T., Akamine A., Joyner A.;
RT  "Expression of growth/differentiation factor 11, a new member of the
    BMP/TGF-beta superfamily during mouse embryogenesis.";
RL  Mech. Dev. 80:185-189(1999).
CC  -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
    IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
CC  PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
    TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN (BY SIMILARITY).
CC  -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC  -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC  -----
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    entities requires a license agreement (See http://www.isb-sib.ch/announce/
    or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF092733; AAD05266.1; -.
DR  HSSP; P18075; 1BMP.
DR  InterPro; IPR001839; TGFb.
DR  InterPro; IPR001111; TGFb_N.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGFb_propeptide; 1.
DR  ProDom; PD000357; TGFb; 1.
DR  SMART; SM00204; TGFb; 1.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
KW  Growth factor; Cytokine; Glycoprotein.
FT  NON TER          1
FT  PROPEP          <1
FT  CHAIN          243 >345 BY SIMILARITY.
FT  DOMAIN          154 159 GROWTH/DIFFERENTIATION FACTOR 11.
FT  DISULFID        257 316 POLY-GLY.
FT  DISULFID        315 315 BY SIMILARITY.
FT  CARBOHYD        38 38 INTERCHAIN (BY SIMILARITY).
FT  NON TER        345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ  SEQUENCE        345 AA; 39094 MW; 81D5B93FED6B0443 CRC64;

Query Match          84.9%; Score 534; DB 1; Length 345;
Best Local Similarity 88.3%; Pred. No. 4.2e-52;
Matches 91; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
```

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Oy 1 DFGDDEHSTSRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEVEFLQKYPHTL 60
Db 243 NLGDDDEHSSSRCCRYPLTVDFEASGWDWIIAPKRYKANYCSGCEVEFLQKYPHTL 302
Oy 61 VHQANPRGSAGPCTPTKMSPIINMLYFNGKEQIYGIKIPAMV 103
Db 303 VQGANPRGSAGPCTPTKMSPIINMLYFNDKQIYGIKIPGMV 345
```

RESULT 14

```

ID  INHB_MOUSE        STANDARD;          PRT;          255 AA.
AC  Q04959; Q61277;
DT  01-FEB-1994 (Rel. 28, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).
GN  INHB.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE OF 1-234 FROM N.A.
RC  STRAIN=CBA X NMRI; TISSUE=Testis;
RX  MEDLINE=95344997; PubMed=7619733;
RA  Rltvos O., Tuuri T., Eramaa M., Sainio K., Hilden K., Saxen L.,
    Gilbert S.;
RT  "Activin disrupts epithelial branching morphogenesis in developing
    glandular organs of the mouse.";
RL  Mech. Dev. 50:229-245(1995).
RN  [2]
RP  SEQUENCE OF 134-255 FROM N.A.
RX  MEDLINE=93321614; PubMed=8330535;
RA  Albano P.M., Groome N., Smith J.C.;
RT  "Activins are expressed in preimplantation mouse embryos and in ES
    and EC cells and are regulated on their differentiation.";
RL  Development 117:711-723(1993).
CC  -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
    RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC  INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
    FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
    GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
    ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
    EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
    SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPOSE THE FUNCTIONS OF
    ACTIVINS.
CC  -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC  INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC  INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC  ACTIVIN A IS A HOMODIMER OF BETA-A.
CC  ACTIVIN B IS A HOMODIMER OF BETA-B.
CC  ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC  -1- TISSUE SPECIFICITY: UTERUS, TESTIS, OVARY, LUNG, KIDNEY, BRAIN,
    C37 EMBRYONIC STEM CELLS, AND POSSIBLY IN LIVER.
CC  -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC  -----
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    or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X83376; CAA58290.1; -.
DR  EMBL; X69620; CAA49326.1; -.
DR  PIR; S31441; S31441.
DR  HSSP; P12643; 3BMP.
DR  MGD; MGI:96571; Inhb.
DR  InterPro; IPR001839; TGFb.
DR  InterPro; IPR001111; TGFb_N.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGFb_propeptide; 1.
DR  ProDom; PD000357; TGFb; 1.
DR  SMART; SM00204; TGFb; 1.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
KW  Growth factor; Hormone; Glycoprotein.
FT  NON TER          1
FT  PROPEP          <1
FT  CHAIN          141 255 INHIBIN BETA B CHAIN.
FT  CHAIN          141 255
```

FT DISULFID 144 152 BY SIMILARITY.
FT DISULFID 151 220 BY SIMILARITY.
FT DISULFID 180 252 BY SIMILARITY.
FT DISULFID 184 254 BY SIMILARITY.
FT DISULFID 219 219 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 135 135 H -> D (IN REF. 2).
SQ SEQUENCE 255 AA; 29178 MW; 2524821DC648D9A9 CRC64;

Query Match 39.4%; Score 248; DB 1; Length 255;
Best Local Similarity 43.2%; Pred. No. 2e-20;
Matches 51; Conservative 17; Mismatches 36; Indels 14; Gaps 6;

QY 3 GLDCDEHSTESRCRYPPLTVDFEAFGW-DWIIAPKRYKANYCSGCEFFVLOKYP----- 56
DB 141 GLECDGRT--SLCGRQGFIDFRLIGWMDWIIAPGTGYGNGCGSCP-AVLAGVPGSAS 197

QY 57 -HTHLVQANPRG-SAGP--CCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGC 109
DB 198 FHTAVVQYRMGRINLPVNSCCIPKLSMSMLYFDEYNIKRDVPMIVEECGCA 255

RESULT 15
DVR1_BRARE STANDARD; PRT; 355 AA.
ID DVR1_BRARE
AC P35621;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DVR-1 protein precursor.
GN Vg1 OR DVR1 OR DVR-1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94009920; PubMed=8405668;
RA Helde K.A., Grunwald D.J.;
RT "The DVR-1 (Vg1) transcript of zebrafish is maternally supplied and
RL distributed throughout the embryo.";
RL Dev. Biol. 159:418-426(1993).
CC -1- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER
CC MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRUCTIVE
CC SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.
CC -1- SUBUNIT: HOMODIMER (PROBABLE).
CC -1- TISSUE SPECIFICITY: ABUNDANT IN OVARIES AND EGGS, AND EQUALLY
CC DISTRIBUTED AMONG ALL BLASTOMERES.
CC -1- DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CYTOPLASM IN
CC JUST-FERTILIZED EGGS. EVENLY PARTITIONED DURING CLEAVAGE AMONG ALL
CC BLASTOMERES. ABSENT IN THE YOLK CELL DURING CLEAVAGE, BLASTULA AND
CC GASTRULA STAGES. DISTRIBUTED HOMOGENEOUSLY AMONG ALL CELLS OF THE
CC GASTRULA.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; U00931; AAC27347.1; .
DR HSSP; P12643; 3BMP.
DR ZFIN; ZDB-GENE-980526-389; dvrl.
DR InterPro; IPR002400; GF_Cys_knot.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.

DR Prodom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF BETA 1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT PROPEP 16 240 POTENTIAL.
FT CHAIN 241 355 DVR-1 PROTEIN.
FT DISULFID 254 320 BY SIMILARITY.
FT DISULFID 283 352 BY SIMILARITY.
FT DISULFID 287 354 BY SIMILARITY.
FT DISULFID 319 319 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 355 AA; 40201 MW; 0ED5B9850EBFB222 CRC64;

Query Match 39.1%; Score 246; DB 1; Length 355;
Best Local Similarity 44.3%; Pred. No. 4.7e-20;
Matches 47; Conservative 16; Mismatches 35; Indels 8; Gaps 3;

QY 11 TESRCR-YPLTVDFEAFGW-DWIIAPKRYKANYCSGCEFFVLOKYPHTH-----LVH 62
DB 249 TPSNVCKRRLIYDFKQVGMQDWIIAPQGYLANVCHGCEPFLSESLNGTVAIIQTLVH 308

QY 63 QANPRGAGPCCCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGC 108
DB 309 SPDPKGTPOPCCVPIKLSPIMLYYDNNVLAHYEDMVVDECGC 354

Search completed: January 31, 2003, 18:21:31
Job time : 9.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 25 Seconds

(without alignments)
898.365 Million cell updates/sec

Title: US-09-620-586B-11

Perfect score: 629

Sequence: 1 DFGIDCDHEHSTESRCRYPL.....KEQIYGIKIPAMVVDRCGCS 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	629	100.0	162	6	Q9TSY2
2	629	100.0	375	6	Q9GM97
3	629	100.0	375	6	Q95J86
4	629	100.0	375	13	Q8UWD8
5	629	100.0	375	13	Q8UWD7
6	624	99.2	375	13	Q98SP0
7	623	99.0	375	13	Q8UWD9
8	621	98.7	375	13	Q8UWE0
9	618	98.3	375	6	Q8WNS6
10	606	96.3	185	6	Q95N11
11	599	95.2	185	6	Q9MZ18
12	570	90.6	389	13	Q90YY0
13	567	90.1	385	13	Q90W05
14	564	89.7	373	13	Q9DDI8
15	564	89.7	373	13	Q90ZD2
16	564	89.7	373	13	Q90ZD1

17	564	89.7	376	13	Q98TB4	Q98tb4 oreochromis
18	564	89.7	376	13	Q90WC9	Q90wc9 morone saxa
19	564	89.7	376	13	Q90WC8	Q90wc8 morone amer
20	563	89.5	373	13	Q90W17	Q90w17 salmo salar
21	562	89.3	376	13	Q90W06	Q90w06 umbrina cir
22	559	88.9	377	13	Q98TB3	Q98tb3 morone chry
23	557	88.6	373	13	Q98UB3	Q98ub3 salvelinus
24	554	88.1	96	13	Q9W759	Q9w759 cairina mos
25	543	86.3	359	13	Q80G53	Q80g53 sparus aura
26	529	84.1	107	6	Q9BG54	Q9bg54 sus scrofa
27	394	62.6	78	6	Q9XS85	Q9xs85 equus caball
28	311	49.4	191	13	Q98TY4	Q98ty4 perca flave
29	302	48.0	104	13	Q90Z79	Q90z79 ictalurus p
30	301.5	47.9	598	5	Q9XZ62	Q9xz62 drosophila
31	301.5	47.9	598	5	Q9V4F4	Q9v4f4 drosophila
32	286	45.5	58	6	Q95MF3	Q95mf3 sus scrofa
33	259	41.2	263	13	Q8QH11	Q8qh11 umbrina cir
34	254	40.4	370	13	Q91350	Q91350 xenopus lae
35	242	38.5	395	13	Q9PMG6	Q9pmg6 anguilla ja
36	241.5	38.4	115	13	Q9DGE9	Q9dge9 cyprinus ca
37	241.5	38.4	393	13	Q90Z61	Q90z61 brachydanio
38	240.5	38.2	392	13	Q9PMR8	Q9pmr8 carassius a
39	239.5	38.1	115	13	Q9DGF1	Q9dgf1 cyprinus ca
40	239.5	38.1	115	13	Q9DGF0	Q9dgf0 cyprinus ca
41	239.5	38.1	115	13	Q9DGE6	Q9dge6 oryzae lat
42	236.5	37.6	138	13	Q9W6T9	Q9w6t9 brachydanio
43	236.5	37.6	354	13	Q9YGV1	Q9ygv1 xenopus lae
44	230.5	36.6	349	5	Q97138	Q97138 brugia mala
45	226.5	36.0	361	5	Q96504	Q96504 branchiosto

ALIGNMENTS

RESULT 1

ID	Q9TSY2	PRELIMINARY;	PRT;	162 AA.
AC	Q9TSY2;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Myostatin (Fragment).			
GN	MSTN.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20078370; PubMed=10612246;			
RA	Stratili A., Kopecky M.;			
RT	"Genomic organization, sequence and polymorphism of the porcine			
RT	myostatin (GDF8; MSTN) gene.";			
RL	Anim. Genet. 30:468-470(1999).			
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			
DR	EMBL; AJ237920; CAB40844.1; -.			
DR	HSSP; P18075; 1BMP.			
DR	InterPro; IPR002400; GF_cysknot.			
DR	InterPro; IPR001839; TGFb.			
DR	InterPro; IPR001111; TGFb_N.			
DR	Pfam; PF00019; TGF-beta; 1.			
DR	Pfam; PF00688; TGFb_propeptide; 1.			
DR	PRINTS; PR00438; GFCYSKNOT.			
DR	PRODOM; PD000357; TGFb; 1.			
DR	SMART; SM00204; TGFb; 1.			
DR	PROSITE; PS00250; TGF_BETA_1; 1.			
KW	Glycoprotein.			
FT	NON_TER			
SQ	SEQUENCE 162 AA; 18290 MW; FE3535334512856E CRC64;			
Query Match 100.0%; Score 629; DB 6; Length 162;				
Best Local Similarity 100.0%; Pred. No. 1e-65;				
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

QY 1 DFGLCDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 60
 DB 54 DFGLCDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 113
 QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNKGKEQIYGIKIPAMVVDRCGCS 109
 DB 114 VHQANPRGSAGPCTPTKMSPINMLYFNKGKEQIYGIKIPAMVVDRCGCS 162

RESULT 2

Q9GM97 PRELIMINARY; PRT; 375 AA.
 AC Q9GM97; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Myostatin.
 GN MSTN.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=THRUOGHRED;
 RA Hosoyama T., Yamanouchi K., Tojo H., Tachi C.;
 RT "Molecular cloning of equine myostatin cDNA and serum level of
 RT myostatin in horse."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AB033541; BAB16046.1; -.
 DR HSSP; P18075; 1BMP.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein.
 SQ SEQUENCE 375 AA; 42736 MW; 6F424ECBE4D936 CRC64;

Query Match 100.0%; Score 629; DB 6; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.4e-65;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 60
 DB 267 DFGLCDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 326
 QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNKGKEQIYGIKIPAMVVDRCGCS 109
 DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNKGKEQIYGIKIPAMVVDRCGCS 375

RESULT 3

Q95J86 PRELIMINARY; PRT; 375 AA.
 AC Q95J86; 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Myostatin.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=GASTROCNEMUS;
 RA Smock S.L., Owen T.A.;
 RT "Cloning of the open reading frame DNA for macaque fascicularis
 RT (Cynomolgus macaque) myostatin (GDF8).";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AY055750; AAL17640.1; -.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
 KW Glycoprotein.
 SQ SEQUENCE 375 AA; 42722 MW; 2149B46AC7D446E7 CRC64;

Query Match 100.0%; Score 629; DB 6; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.4e-65;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 60
 DB 267 DFGLCDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 326
 QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNKGKEQIYGIKIPAMVVDRCGCS 109
 DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNKGKEQIYGIKIPAMVVDRCGCS 375

RESULT 4

Q8UWD8 PRELIMINARY; PRT; 375 AA.
 AC Q8UWD8; 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Myostatin.
 GN MSTN.
 OS Columba livia (Domestic pigeon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
 OX NCBI_TaxID=8932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
 RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
 RT Duck, Goose, Pigeon and Quail.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF440863; AAL35277.1; -.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
 SQ SEQUENCE 375 AA; 42739 MW; 88296F0AE779476E CRC64;

Query Match 100.0%; Score 629; DB 13; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.4e-65;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLCDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 60
 DB 267 DFGLCDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 326
 QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNKGKEQIYGIKIPAMVVDRCGCS 109
 DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNKGKEQIYGIKIPAMVVDRCGCS 375

RESULT 5

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Q8UWD7 PRELIMINARY; PRT; 375 AA.
ID Q8UWD7;
AC Q8UWD7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Coturnix chinensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=46218;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440864; AAL35278.1; -.
DR InterPro; IPR001839; TGFb.N.
DR InterPro; IPR001839; TGFb.N.
DR Pfam; PF00688; TGFb_beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42721 MW; B893B1A42DE0725 CRC64;

Query Match 100.0%; Score 629; DB 13; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.4e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCPTPTKSPINMLYFNGKEQIIYGIKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKSPINMLYFNGKEQIIYGIKIPAMVVDRCGCS 375

RESULT 6
Q8SP0 PRELIMINARY; PRT; 375 AA.
ID Q8SP0;
AC Q8SP0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Yang W., Zhu D.;
RT "Genomic structure and expression of the chicken GDF-8 during
RT development."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF346599; AAK18000.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR002048; EF_HAND.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.

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DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42717 MW; D980E286426E4D4F CRC64;

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Query Match 99.2%; Score 624; DB 13; Length 375;
Best Local Similarity 99.1%; Pred. No. 9.2e-65;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 DFGLDCEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCPTPTKSPINMLYFNGKEQIIYGIKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKSPINMLYFNGKEQIIYGIKIPAMVVDRCGCS 375

RESULT 7
Q8UWD9 PRELIMINARY; PRT; 375 AA.
ID Q8UWD9;
AC Q8UWD9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8843;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440862; AAL35276.1; -.
DR InterPro; IPR002048; EF_HAND.
DR InterPro; IPR001839; TGFb.N.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42667 MW; 57DDE49D3AA2978C CRC64;

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Query Match 99.0%; Score 623; DB 13; Length 375;
Best Local Similarity 99.1%; Pred. No. 1.2e-64;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 DFGLDCEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCPTPTKSPINMLYFNGKEQIIYGIKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPTKSPINMLYFNGKEQIIYGIKIPAMVVDRCGCS 375

RESULT 8
Q8UWE0 PRELIMINARY; PRT; 375 AA.
ID Q8UWE0;
AC Q8UWE0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

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DE Myostatin.
GN MSTN.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF40861; AAL35275.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42524 MW; 0EC27616C202F5E6 CRC64;

Query Match 98.7%; Score 621; DB 13; Length 375;
Best Local Similarity 99.1%; Pred. No. 2.1e-64;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 326

QY 61 VHQANPRGSAGPCTPTKMSPIINMLYFNKGKQIIGKIPAMVVDRCGS 109
DB 327 VHQANPRGSAGPCTPTKMSPIINMLYFNKGKQIIGKIPAMVVDRCGS 375

RESULT 9
Q8WNS6 PRELIMINARY; PRT; 375 AA.
AC Q8WNS6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myostatin.
GN GDF8.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Shibata M., Muramoto T., Aikawa K.;
RT "Genomic organization and sequence of the myostatin gene in bovine."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB076403; BAB79498.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42524 MW; 0EC27616C202F5E6 CRC64;

Query Match 98.3%; Score 618; DB 6; Length 375;
Best Local Similarity 98.2%; Pred. No. 4.6e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 326

DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 326

QY 61 VHQANPRGSAGPCTPTKMSPIINMLYFNKGKQIIGKIPAMVVDRCGS 109
DB 327 VHQANPRGSAGPCTPTKMSPIINMLYFNKGKQIIGKIPAMVVDRCGS 375

RESULT 10
Q95N11 PRELIMINARY; PRT; 185 AA.
AC Q95N11;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN MSTN.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Lian Z., Pan Q., Chen H., Jin H., Li N.;
RT "Cloning of intron 2 of the myostatin gene in goat."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AY032689; AAK49790.1; -.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb.N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW glycoprotein.
FT NON_TER 1 1
FT NON_TER 185 185
SQ SEQUENCE 185 AA; 20953 MW; 03675B386E9D64D4 CRC64;

Query Match 96.3%; Score 606; DB 6; Length 185;
Best Local Similarity 97.2%; Pred. No. 5.7e-63;
Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 60
DB 79 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 138

QY 61 VHQANPRGSAGPCTPTKMSPIINMLYFNKGKQIIGKIPAMVVDRCGS 107
DB 139 VHQANPRGSAGPCTPTKMSPIINMLYFNKGKQIIGKIPAMVVDRCGS 185

RESULT 11
Q9MZ18 PRELIMINARY; PRT; 185 AA.
AC Q9MZ18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN MSTN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Lian Z., Jin H., Li N.;
RT "Cloning of intron 2 of the myostatin gene in sheep."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF266758; AAF78069.1; -.

DR	HSSP; P12643; 3BMP.			
DR	InterPro; IPR001839; TGFb.			
DR	InterPro; IPR001111; TGFb N.			
DR	Pfam; PF00019; TGF-beta; 1.			
DR	Pfam; PF00688; TGFb propeptide; 1.			
DR	ProDom; PD000357; TGFb; 1.			
DR	SMART; SM00204; TGFb; 1.			
DR	PROSITE; PS00250; TGF_BETA_1; 1.			
KW	Glycoprotein.			
FT	NON_TER	1		
FT	NON_TER	185	185	
SQ	SEQUENCE	185 AA;	20923 MW;	BA9634203A52850 CRC64;

Query Match	95.2%;	Score 599;	DB 6;	Length 185;
Best Local Similarity	96.3%;	Pred. No. 3.8e-62;		
Matches 103; Conservative	2;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 DFGDDEHSTESRCRRPLTVDFEAFGDMWIIAPKRYANYCSGECEFEVLQKYPHTL 60

Db 79 DFGDDCDVHSTESRCRRPLTVDFEAFGDMWIIAPKRYANYCSGECEFEVLQKYPHTL 138

QY 61 VHQANPRGSAGBPCCCTPTKMSPINMLYENGKQIIYKGIAPANVVDRCG 107

Db 139 VHQANPKGSAGBPCCCTPTKMSPINMLYFNGKQIIYKGIQGMVVVDRCG 185

RESULT 12	
Q90YY0	
ID Q90YY0	PRELIMINARY;
*****	PRT; 389 AA

DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Myostatin.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Kocabas A.M., Liu Z.J.;
RT "Molecular characterization and expression of the myostatin gene from
RL channel catfish (*Ictalurus punctatus*).";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AF396747; AAK84666.1; -.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 389 AA; 43600 MW; 569FB952B7B3E173 CRC64;

Query Match	90.6%;	Score 570;	DB 13;	Length 389;
Best Local Similarity	90.7%;	Pred. No. 2e-58;		
Matches 97; Conservative	8;	Mismatches 2;	Indels 0;	Gaps 0;

QY	3	GLDDEHSTESRCCRYPLTVDFEAFEGMWIIAPKRYKANYCSGECEFFVLQKYPHTLVH	62
Dd	283	GLDDDENSSSRRCRYPLTVDFEFDMWIIAPKRYKANYCSGECDYVHLQKYPHTLVN	342
QY	63	QANPRGSAGPCCTPTKMSPINMLYFNGKEQIITYGIIPAMVVDRCGCS	109
Dd	343	KANPRGTAGPCCCTPTKMSPINMLYFNGKEQIITYGIIPSMVVDRCGS	389

RESULT 13		
Q90W05		
ID Q90W05	PRELIMINARY;	PRT; 385 AA.
AC Q90W05;		

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DT 01-DEC-2001 (Tremblurel. 19, Created)
DT 01-DEC-2001 (Tremblurel. 19, last sequence update)
DT 01-JUN-2002 (Tremblurel. 21, last annotation update)
DE Myostatin.
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RA Maccatrozzo L., Bargelloni L., Radaelli G., Mascarello F.,
RA Patarnello T.;
RT "Characterization of the myostatin gene in the gilthead seabream,
RT Sparus aurata: sequence, genomic structure, and expression pattern.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF258448; AAK53545.1; -.
DR EMBL; AF258447; AAK53544.1; -.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 385 AA; 43704 MW; 18F902CE325A3916 CRC64;

```

Query Match	90.1%;	Score 567;	DB 13;	Length 385;
Best Local Similarity	89.9%;	Pred. No. 4.4e-58;		
Matches 98;	Conservative	6;	Mismatches 5;	Indels 0;
				Gaps 0;

[illegible]

RESULT 14	
Q9DD18	
ID Q9DD18	PRELIMINARY; PRT; 373 AA

DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBrel. 18, last sequence update)
DT 01-JUN-2002 (TREMBrel. 21, last annotation update)
DE Myostatin precursor.
GN GDF-8.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;

RP SEQUENCE FROM N.A.
RA Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.,
RT "The two myostatin genes of Atlantic salmon (*Salmo salar*) are
RT expressed in a variety of tissues.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.,
Andersen O.;
"The two myostatin genes of Atlantic salmon (*Salmo salar*) are
expressed in a variety of tissues.";
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 32 Seconds
(without alignments)
453.885 Million cell updates/sec

Title: US-09-620-586B-11

Perfect score: 629
Sequence: 1 DFGLDCEHSTESRCRYPL.....KEQIIYKIPAMVDRGCS 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.101002.*

1: /SIDS2/gcgdata/geneseq/geneqp-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneqp-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneqp-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneqp-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneqp-emb1/AA1984.DAT:*
6: /SIDS2/gcgdata/geneqp-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneqp-emb1/AA1986.DAT:*
8: /SIDS2/gcgdata/geneqp-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneqp-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneqp-emb1/AA1989.DAT:*
11: /SIDS2/gcgdata/geneqp-emb1/AA1990.DAT:*
12: /SIDS2/gcgdata/geneqp-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneqp-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneqp-emb1/AA1993.DAT:*
15: /SIDS2/gcgdata/geneqp-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneqp-emb1/AA1995.DAT:*
17: /SIDS2/gcgdata/geneqp-emb1/AA1996.DAT:*
18: /SIDS2/gcgdata/geneqp-emb1/AA1997.DAT:*
19: /SIDS2/gcgdata/geneqp-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneqp-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneqp-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneqp-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	629	100.0	109	22	AAB20141	Human growth diffe
2	629	100.0	109	23	AAM51935	Human TGFbeta prot
3	629	100.0	126	15	AAR63161	Mouse growth diffe
4	629	100.0	126	19	AAW69883	Murine growth diffe
5	629	100.0	126	20	AAV15386	C-terminal region
6	629	100.0	126	22	AAB73182	Murine GDF-8 #1.
7	629	100.0	130	22	AAB73189	Rat GDF-8, Rattus
8	629	100.0	160	22	AAB20153	Growth differentiation
9	629	100.0	226	22	AAB73188	Chicken GDF-8, Ga
10	629	100.0	254	22	AAB20152	Growth differentiation

11	629	100.0	362	22	AAB20132	Turkey growth diff
12	629	100.0	374	23	AAU75623	Chicken promyostat
13	629	100.0	375	15	AAR63160	Human growth diffe
14	629	100.0	375	19	AAW69888	Chicken growth dif
15	629	100.0	375	19	AAW69891	Pig growth diffe
16	629	100.0	375	19	AAW69885	Human growth diffe
17	629	100.0	375	19	AAW65460	Human growth diffe
18	629	100.0	375	20	AAV33838	Amino acid sequenc
19	629	100.0	375	20	AAV33839	Amino acid sequenc
20	629	100.0	375	20	AAV33840	Amino acid sequenc
21	629	100.0	375	20	AAV33841	Amino acid sequenc
22	629	100.0	375	20	AAV33843	Amino acid sequenc
23	629	100.0	375	20	AAV33844	Amino acid sequenc
24	629	100.0	375	20	AAV33837	Amino acid sequenc
25	629	100.0	375	20	AAV33938	Amino acid sequenc
26	629	100.0	375	20	AAV33932	Amino acid sequenc
27	629	100.0	375	20	AAV33935	Amino acid sequenc
28	629	100.0	375	20	AAV31189	Human GDF-8 protei
29	629	100.0	375	20	AAV31192	Chicken GDF-8 prot
30	629	100.0	375	20	AAV31194	Turkey GDF-8 prote
31	629	100.0	375	20	AAW97887	Human myostatin.
32	629	100.0	375	21	AAB21087	Human GDF-8. Homo
33	629	100.0	375	21	AAV92035	Human growth diffe
34	629	100.0	375	21	AAV77566	Human growth diffe
35	629	100.0	375	22	AAB73187	Human GDF-8 #2. H
36	629	100.0	375	22	AAB20131	Human growth diffe
37	629	100.0	375	22	AAB20133	Chicken growth dif
38	629	100.0	375	22	AAB20138	Pig growth diffe
39	629	100.0	375	23	AAE18659	Human promyostatin
40	629	100.0	375	23	AAE18662	Chicken promyostat
41	629	100.0	375	23	AAE18665	Porcine promyostat
42	629	100.0	375	23	AAE18667	Meleagris gallopav
43	629	100.0	375	23	AAU75620	Human promyostatin
44	629	100.0	375	23	AAU75626	Porcine promyostat
45	629	100.0	375	23	AAU75628	Turkey promyostati

ALIGNMENTS

RESULT 1	
1	AAB20141 standard; Protein; 109 AA.
ID	AAB20141
AC	AAB20141;
XX	
DT	30-APR-2001 (first entry)
XX	
DE	Human growth differentiation factor 8 C-terminal region.
XX	
KW	Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
KW	vaccine; muscle; meat; cachexia; cardiant; human; mutant; mutein.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200105820-A2.
XX	
PD	25-JAN-2001.
XX	
PF	20-JUL-2000; 2000WO-DK00413.
XX	
PR	20-JUL-1999; 99DK-0001014.
PR	26-JUL-1999; 99US-0145275.
XX	
PA	(MEBI-) M & E BIOTECH AS.
XX	
PI	Halikier T, Mouritsen S, Klysner S;
XX	
DR	WPI; 2001-112680/12.
XX	
PT	Increasing the muscle mass of animals used in meat production by down
PT	regulating growth differentiation factor 8 (GDF-8) activity in the

PT animal through induction of anti-GDF-8 antibody production -
XX
PS Claim 17; Page 93-94; 110pp; English.
XX

CC The present sequence comprises the 109 amino acid residue
CC C-terminal region of human growth differentiation factor 8
CC (GDF-8), i.e. residues 267-375 of the full-length protein (see
CC AAB20131). The homodimer of this region is thought to be the
CC biologically active form of GDF-8. It is an object of the
CC invention to produce a recombinant therapeutic vaccine capable of
CC effecting down-regulation of GDF-8 in order to increase the muscle
CC growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)
CC are provided that are capable of breaking autotolerance against
CC autologous GDF-8. These comprise the C-terminal portion of human
CC GDF-8 in which a portion of the native sequence is replaced by a
CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
CC P2 or P30. The high number (9) of Cys residues in the C-terminal
CC region limits the possible sites in which the T-cell epitope can be
CC positioned without major disturbance of the native 3-dimensional
CC structure of the protein. Nucleic acids encoding the GDF-8 variants
CC can be used for genetic immunisation of the animals. Down-regulation
CC of GDF-8 activity can increase muscle mass by up to at least 45% in
CC cattle, pigs and poultry used for meat production, reducing the need
CC for antibiotic feed-additives. Anti-GDF8 vaccines can be used to
CC treat human diseases such as cancer cachexia where muscle atrophy is
CC pronounced and for patients suffering from acute and chronic heart
CC failure.

XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 629; DB 22; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.8e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGLCDSEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVLOKYPHTL 60
DB 1 DFGLCDSEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVLOKYPHTL 60

OY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109
DB 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109

RESULT 2
AAM51935

ID AAM51935 standard; protein; 109 AA.

XX
AC AAM51935;

DT 01-FEB-2002 (first entry)

DE Human TGFbeta protein superfamily protein GDF8.

KW Human; TGFbeta; transforming growth factor beta; mutant; antagonist;
KW agonist; ectopic bone formation; psoriasis; muscular atrophy; scar;
KW formation; fibrosis; cirrhosis; osteopathic; antipsoriatic;
KW antifibrotic; hepatotropic; vulnery; GDF8.

XX
OS Homo sapiens.

PN DE10026713-A1.

PD 06-DEC-2001.

PF 30-MAY-2000; 2000DE-1026713.

PR 30-MAY-2000; 2000DE-1026713.

PA (SEBA/) SEBALD W.

PI Sebald W, Nickel J;

DR WPI; 2002;042559/06.

XX
PT New mutein of transforming growth factor-beta superfamily protein,
PT useful for treating or preventing e.g. ectopic bone formation, competes
PT for receptor binding -
XX

PS Disclosure; Fig 6; 54pp; German.

XX
CC The present invention relates to muteins of a chain of a protein which,
CC when in the form of a homodimer, has antagonistic or partial agonistic
CC activity, and where the mutation results in the protein binding with low
CC affinity to its receptor. The protein is a member of the transforming
CC growth factor beta (TGFbeta) superfamily. The mutant sequences of the
CC invention can be used in the treatment of diseases associated with the
CC overexpression of TGFbeta family proteins, including ectopic bone
CC formation, psoriasis, muscular atrophy, scar formation, fibrosis and
CC cirrhosis. The present sequence is the human GDF8 protein.

XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 629; DB 23; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.8e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGLCDSEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVLOKYPHTL 60
DB 1 DFGLCDSEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVLOKYPHTL 60

OY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109
DB 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109

RESULT 3
AAR63161

ID AAR63161 standard; Protein; 126 AA.

XX
AC AAR63161;

DT 23-JUN-1995 (first entry)

DE Mouse growth differentiation factor-8 partial sequence.

KW Growth differentiation factor-8; GDF-8; cell proliferation;
KW adipocyte; obesity; transforming growth factor-beta.

XX
OS Mus musculus.

PN W09421681-A.

PD 29-SEP-1994.

PF 18-MAR-1994; 94WO-US03019.

PR 19-MAR-1993; 93US-0033923.

PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.

PI Lee S, Mcpherron AC;

DR WPI; 1994-316943/39.

DR Q-PSDB; Q76380.

PT New growth differentiation factor 8 - useful for treatment and
PT diagnosis of cell proliferative disorders esp. of muscle.

PS Disclosure; Page 41; 84pp; English.

CC GDF-8 can be used to maintain cells before transplantation; to
CC improve efficiency of cell fusion and to treat obesity or diseases
CC related to abnormal adipocyte proliferation.

SQ Sequence 126 AA;

Query Match 100.0%; Score 629; DB 15; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.3e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGDDEHSTESRCRYPPLTVDFEAFGWDWITAPKRYKANYSGCECFVFLQKYPHTL 60
DB 18 DFGDDEHSTESRCRYPPLTVDFEAFGWDWITAPKRYKANYSGCECFVFLQKYPHTL 77
OY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 109
DB 78 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 126

RESULT 4

AAW69883
ID AAW69883 standard; Protein; 126 AA.

XX AC AAW69883;

XX DT 07-DEC-1998 (first entry)

XX DE Murine growth differentiation factor-8 C-terminal fragment.

XX KW Growth differentiation factor-8; GDF-8; mouse; transgenic animal;
XX KW transforming growth factor-beta; muscle; meat; inhibitor; obesity;
XX KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
XX KW therapy.

XX OS Mus sp.

XX FH Key Location/Qualifiers

FT Cleavage-site 13..14
FT Cleavage-site 16..17
FT Protein 17..126

FT /note= "mature polypeptide"

XX PN WO9833887-A1.

XX PD 06-AUG-1998.

XX PF 05-FEB-1998; 98WO-US02479.

XX PR 23-MAY-1997; 97US-0862445.

XX PR 05-FEB-1997; 97US-0795071.

XX PR 28-APR-1997; 97US-0847910.

XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX PI Lee S, McPherron AC;

XX DR WPI; 1998-437444/37.

XX DR N-PSDB; AAV45809.

XX PT Transgenic animals with gene for growth differentiation factor-8

XX PT also use of GDF-8 inhibitors for treating cancer, obesity,
XX PT neuromuscular disease

XX PS Example 2; Page 58; 125pp; English.

XX CC This is the amino acid sequence of the C-terminal portion of mouse
XX CC growth differentiation factor-8 (GDF-8), a novel member of the
XX CC transforming growth factor-beta superfamily that appears to relate
XX CC to various cell proliferative disorders, especially those involving
XX CC muscle, nerve and adipose tissue. The sequence was deduced from a
XX CC partial genomic clone (see AAV45809). A full-length sequence (see
XX CC AAW30689) has been deduced from a cDNA clone (see AAV42113). The
XX CC invention provides novel mammalian and avian GDF-8 proteins (see
XX CC AAW69883-92). A transgenic non-human animal is claimed in which
XX CC GDF-8 expression is disrupted or interfered with. Also claimed
XX CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
XX CC from these animals; (2) method for increasing muscle mass in
XX CC animals by administering an antibody (Ab) that binds to GDF-8; (3)

CC inhibiting the action of GDF-8 by treating foetal or adult muscle
CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
CC acid encoding a GDF-8 protein truncated by loss of the C-terminal
CC active fragment. The transgenic animals have increased muscle mass
CC and for poultry reduced cholesterol contents. Method (3) is used
CC to treat muscle wasting or neuromuscular diseases, muscular atrophy
CC and aging, particularly muscular dystrophy, spinal cord or
CC traumatic injuries, congestive or obstructive lung disease, AIDS
CC and cachexia. Method (4) is used to treat cancer of muscle,
CC connective tissue and bone, or obesity. Also (not claimed) GDF-8
CC can be used to maintain myoblasts intended for transplanting or to
CC improve efficiency of fusion. Ab can be used to detect and
CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
CC also for immunotherapy and in vivo imaging.

XX SQ Sequence 126 AA;

Query Match 100.0%; Score 629; DB 19; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.3e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGDDEHSTESRCRYPPLTVDFEAFGWDWITAPKRYKANYSGCECFVFLQKYPHTL 60
DB 18 DFGDDEHSTESRCRYPPLTVDFEAFGWDWITAPKRYKANYSGCECFVFLQKYPHTL 77
OY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 109
DB 78 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 126

RESULT 5

AAV15386
ID AAV15386 standard; Protein; 126 AA.

XX AC AAV15386;

XX DT 08-DEC-1999 (first entry)

XX DE C-terminal region of mouse Growth Differentiation Factor-8 (GDF-8).

XX KW growth differentiation factor; tissue growth; muscle growth;
XX KW cell differentiation; animal feed; muscle disorder;
XX KW bone degeneration; nerve degeneration; GDF-8; development;
XX KW transforming growth factor beta; TGF-beta.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Cleavage-site 13..14
FT Cleavage-site /label= Potential_proteolytic_cleavage_site
FT Cleavage-site 16..17
FT /label= Potential_proteolytic_cleavage_site
FT /note= "cleavage generates mature protein"

XX PN WO9940181-A1.

XX PD 12-AUG-1999.

XX PF 05-FEB-1999; 99WO-US02511.

XX PR 28-JUL-1998; 98US-0124180.

XX PR 05-FEB-1998; 98US-0019070.

XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX PI Lee S, McPherron AC;

XX DR WPI; 1999-494289/41.

XX DR N-PSDB; AAZ06446.

XX PT New differentiation factor useful for treating neurodegenerative

XX PT diseases

PS Example 2; Fig 2a; 138pp; English.

XX This is the amino acid sequence of the C-terminal region of the GDF-8
CC precursor protein. The predicted GDF-8 sequence contains two potential
CC proteolytic processing sites.
CC Cleavage of the precursor at the second of these sites would generate
CC a mature C terminal fragment 109 amino acids in length with a predicted
CC molecular weight of 12,400.
CC GDF-8 has been shown to result in increased bone and muscle mass (such
CC as ribs) when expressed in reduced amounts. GDF-8 minus transgenic
CC animals and forms of animal feed that can inhibit/reduce production of
CC GDF-8 are of commercial interest.
CC GDF-8 expression may also have a role in the therapy of abnormal growth
CC of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8
CC antisense molecule or dominant negative polypeptide could be used with
CC foetal or adult muscle cells, bone cells or progenitor cells. These
CC agents can be administered to a patient suffering from a disorder such
CC as muscle wasting disease, neuro muscular disorder, muscle atrophy,
CC osteoporosis, bone degenerative diseases, obesity or other adipocyte
CC cell disorders, and aging for example.

XX Sequence 126 AA;

Query Match 100.0%; Score 629; DB 20; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.3e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 18 DFGLDCEHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 77

QY 61 VHOANPRGSAGPCTPTKMSPIINMLYFNKGKQIIYGKIPAMVVDRCGCS 109
DB 78 VHOANPRGSAGPCTPTKMSPIINMLYFNKGKQIIYGKIPAMVVDRCGCS 126

RESULT 6

AAB73182 standard; Protein; 126 AA.

XX AAB73182;

DT 11-MAY-2001 (first entry)

XX Murine GDF-8 #1.

KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW muscular dystrophy; musculodegenerative disease; tissue repair;
KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease.

XX Mus sp.

XX WO200112777-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22884.

XX 19-AUG-1999; 99US-0378238.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Lee S, McPherron AC;

XX WPI; 2001-211209/21.

XX N-PSDB; AAF63547.

PT New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia -

XX Example 2; Fig 2; 124pp; English.

XX The present invention relates to growth differentiation factor-8 (GDF-8)
CC coding sequences and proteins. The present sequence is a GDF-8 protein,
CC which was isolated in the present invention. GDF-8 is useful for treating
CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
CC muscular dystrophy), musculodegenerative diseases or in tissue repair due
CC to trauma, obesity and disorders related to abnormal proliferation of
CC adipocytes. GDF-8 is also useful for treating malignancies of the various
CC organ systems, particularly cells in muscle or adipose tissues and in
CC gene therapy for the treatment of cell proliferative or immunological
CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
CC treating muscle wasting disease, neuromuscular disorder, spinal cord
CC injury, traumatic injury, congestive obstructive pulmonary disease
CC (COPD), AIDS or cachexia.

XX Sequence 126 AA;

Query Match 100.0%; Score 629; DB 22; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.3e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 18 DFGLDCEHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 77

QY 61 VHOANPRGSAGPCTPTKMSPIINMLYFNKGKQIIYGKIPAMVVDRCGCS 109
DB 78 VHOANPRGSAGPCTPTKMSPIINMLYFNKGKQIIYGKIPAMVVDRCGCS 126

RESULT 7

AAB73189 standard; Protein; 130 AA.

XX AAB73189;

DT 11-MAY-2001 (first entry)

XX Rat GDF-8.

KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW muscular dystrophy; musculodegenerative disease; tissue repair;
KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease.

XX Rattus sp.

XX WO200112777-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22884.

XX 19-AUG-1999; 99US-0378238.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Lee S, McPherron AC;

XX WPI; 2001-211209/21.

XX N-PSDB; AAF63555.

PT New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia -

XX Example 9; Fig 2; 124pp; English.

XX The present invention relates to growth differentiation factor-8 (GDF-8)

CC coding sequences and proteins. The present sequence is a GDF-8 protein,
 CC which was isolated in the present invention. GDF-8 is useful for treating
 CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
 CC muscular dystrophy), musculoskeletal diseases or in tissue repair due
 CC to trauma, obesity, and disorders related to abnormal proliferation of
 CC adipocytes. GDF-8 is also useful for treating malignancies of the various
 CC organ systems, particularly cells in muscle or adipose tissues and in
 CC gene therapy for the treatment of cell proliferative or immunological
 CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
 CC treating muscle wasting disease, neuromuscular disorder, spinal cord
 CC injury, traumatic injury, congestive obstructive pulmonary disease
 CC (COPD), AIDS or cachexia.
 CC
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 629; DB 22; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.4e-60;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
 DB 22 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 81
 QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109
 DB 82 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 130
 RESULT 8
 AAB20153
 ID AAB20153 standard; Protein; 160 AA.
 AC AAB20153;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Growth differentiation factor 8 Autovac construct GDF-8 ext.
 XX
 KW Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
 KW T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
 KW cardiant; human; mutant; mutein.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Clostridium tetani.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT 1..15
 FT /note= "identical to residues 215-230 of human
 FT GDF-8"
 FT Region
 FT 16..36
 FT /note= "tetanus toxoid P30 epitope"
 FT Region
 FT 37..51
 FT /note= "tetanus toxoid P2 epitope"
 FT Region
 FT 52..160
 FT /note= "identical to residues 267-375 of human
 FT GDF-8"
 FT Misc-difference 124
 FT /note= "Cys-124 may be substituted by Ser to avoid
 FT disulfide bond formation"
 FT Misc-difference 141..142
 FT /note= "optionally replaced by Glu-Gly"
 XX
 PN WO200105820-A2.
 XX
 PD 25-JAN-2001.
 XX
 PF 20-JUL-2000; 2000WO-DK00413.
 XX
 PR 20-JUL-1999; 99DK-0001014.
 PR 26-JUL-1999; 99US-0145275.
 XX
 PA (MEBI-) M & B BIOTECH AS.

XX
 PI Halkier T, Mouritsen S, Klysner S;
 XX WPI; 2001-112680/12.
 DR
 XX
 PT Increasing the muscle mass of animals used in meat production by down
 PT regulating growth differentiation factor 8 (GDF-8) activity in the
 PT animal through induction of anti-GDF-8 antibody production -
 XX
 PS Example 1; Page 107-108; 110pp; English.
 XX
 CC The present sequence is that of Autovac construct GDF-8 ext,
 CC which consists of the C-terminal 160 amino acids of human growth
 CC differentiation factor 8 (GDF-8, see AAF20131) with residues 16-36
 CC substituted by the promiscuous tetanus toxin T-cell epitope P30 (see
 CC AAB20144) and residues 37-51 substituted by tetanus toxin T-cell
 CC epitope P2 (see AAB20143). It is an object of the invention to
 CC produce a recombinant therapeutic vaccine that is capable of effecting
 CC down-regulation of GDF-8 in order to increase the muscle growth
 CC rate of farm animals. The vaccines (see AAB20145-53) are capable
 CC of breaking autotolerance against autologous GDF-8. They comprise
 CC the C-terminal portion of human GDF-8 in which a portion of the
 CC native sequence is replaced by a T-cell epitope such as P30, with
 CC minimal disturbance of the authentic 3-dimensional structure of
 CC the protein. Nucleic acids encoding the GDF-8 variants can be used
 CC for genetic immunisation of the animals. Down-regulation of GDF-8
 CC activity can increase muscle mass by up to at least 45% in cattle,
 CC pigs and poultry used for meat production, reducing the need for
 CC antibiotic feed-additives. Anti-GDF8 vaccines can be used to
 CC treat human diseases such as cancer cachexia where muscle atrophy is
 CC pronounced and for patients suffering from acute and chronic heart
 CC failure.
 CC
 SQ Sequence 160 AA;
 Query Match 100.0%; Score 629; DB 22; Length 160;
 Best Local Similarity 100.0%; Pred. No. 4.2e-60;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
 DB 52 DFGLDCEHSTESRCRYPYLVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 111
 QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109
 DB 112 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 160
 RESULT 9
 AAB73188
 ID AAB73188 standard; Protein; 226 AA.
 AC AAB73188;
 XX
 DT 11-MAY-2001 (first entry)
 XX
 DE Chicken GDF-8.
 XX
 KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
 KW muscular dystrophy; musculoskeletal disease; tissue repair;
 KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
 KW traumatic injury; congestive obstructive pulmonary disease.
 XX
 OS Gallus gallus.
 XX
 PN WO200112777-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22884.
 PF 19-AUG-1999; 99US-0178238.
 XX
 PR

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XX PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX PI Lee S, McPherron AC;
XX DR WPI; 2001-211209/21.
XX DR N-PSDB; AAF63554.
XX PT New substantially purified growth differentiation factor-8 polypeptide,
XX PT useful for treating muscle wasting disease, obesity, muscular
XX PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
XX PT and cachexia
XX PS Example 9; Fig 2; 124pp; English.
XX CC The present invention relates to growth differentiation factor-8 (GDF-8)
XX CC coding sequences and proteins. The present sequence is a GDF-8 protein,
XX CC which was isolated in the present invention. GDF-8 is useful for treating
XX CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
XX CC muscular dystrophy), musculoskeletal diseases or in tissue repair due
XX CC to trauma, obesity and disorders related to abnormal proliferation of
XX CC adipocytes. GDF-8 is also useful for treating malignancies of the various
XX CC organ systems, particularly cells in muscle or adipose tissues and in
XX CC gene therapy for the treatment of cell proliferative or immunological
XX CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
XX CC treating muscle wasting disease, neuromuscular disorder, spinal cord
XX CC injury, traumatic injury, congestive obstructive pulmonary disease
XX CC (COPD), AIDS or cachexia.
XX SQ Sequence 226 AA;
XX
XX Query Match 100.0%; Score 629; DB 22; Length 226;
XX Best Local Similarity 100.0%; Pred. No. 6.2e-60;
XX Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYSGECEFVFLQKYPHTL 60
DB 118 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYSGECEFVFLQKYPHTL 177
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGKEQIITGKIPAMVVDRCGCS 109
DB 178 VHOANPRGSAGPCCPTPTKMSPINMLYFNGKEQIITGKIPAMVVDRCGCS 226
XX
XX RESULT 10
XX AAB20152
XX ID AAB20152 standard; Protein; 254 AA.
XX AC AAB20152;
XX DT 30-APR-2001 (first entry)
XX DB Growth differentiation factor 8 Autovac construct GDF-8 dimer.
XX KW Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
XX KW T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
XX KW cardiant; human; mutant; mutein.
XX OS Chimeric - Homo sapiens.
XX OS Chimeric - Clostridium tetani.
XX OS Synthetic.
XX FH Key
XX FT Location/Qualifiers
XX FT 1..109
XX FT /note= "109 C-terminal residues of human GDF-8"
XX FT Region
XX FT 110..124
XX FT /note= "tetanus toxoid P2 epitope"
XX FT Region
XX FT 125..145
XX FT /note= "tetanus toxoid P30 epitope"
XX FT Region
XX FT 146..254
XX FT /note= "109 C-terminal residues of human GDF-8"
XX FT Misc-difference 90..91
XX FT /note= "optionally replaced by Glu-Gly"

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XX FT Misc-difference 235..236
XX FT /note= "optionally replaced by Glu-Gly"
XX PN WO200105820-A2.
XX PD 25-JAN-2001.
XX PF 20-JUL-2000; 2000WO-DK00413.
XX PR 20-JUL-1999; 99DK-0001014.
XX PR 26-JUL-1999; 99US-0145275.
XX PA (MEBI-) M & E BIOTECH AS.
XX PI Halkier T, Mouritsen S, Klynsner S;
XX DR WPI; 2001-112680/12.
XX PT Increasing the muscle mass of animals used in meat production by down
XX PT regulating growth differentiation factor 8 (GDF-8) activity in the
XX PT animal through induction of anti-GDF-8 antibody production
XX PS Example 1; Page 105-106; 110pp; English.
XX CC The present sequence is that of Autovac construct GDF-8 dimer
XX CC comprising 2 copies of the 109-amino acid C-terminal region of human
XX CC growth differentiation factor 8 (GDF-8, see AAF20141) covalently
XX CC connected through the P2 and P30 T-cell epitopes (see AAB20143-44)
XX CC of tetanus toxin. It is an object of the invention to produce a
XX CC recombinant therapeutic vaccine that is capable of effecting
XX CC down-regulation of GDF-8 in order to increase the muscle growth
XX CC rate of farm animals. The vaccines (see AAB20145-53) are capable
XX CC of breaking autotolerance against autologous GDF-8. They comprise
XX CC the C-terminal portion of human GDF-8 in which a portion of the
XX CC native sequence is replaced by a T-cell epitope such as P30, with
XX CC minimal disturbance of the authentic 3-dimensional structure of
XX CC the protein. Nucleic acids encoding the GDF-8 variants can be used
XX CC for genetic immunisation of the animals. Down-regulation of GDF-8
XX CC activity can increase muscle mass by up to at least 45% in cattle,
XX CC pigs and poultry used for meat production, reducing the need for
XX CC antibiotic feed-additives. Anti-GDF8 vaccines can be used to
XX CC treat human diseases such as cancer cachexia where muscle atrophy is
XX CC pronounced and for patients suffering from acute and chronic heart
XX CC failure.
XX SQ Sequence 254 AA;
XX
XX Query Match 100.0%; Score 629; DB 22; Length 254;
XX Best Local Similarity 100.0%; Pred. No. 7e-60;
XX Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYSGECEFVFLQKYPHTL 60
DB 146 DFGLCDDEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYSGECEFVFLQKYPHTL 205
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGKEQIITGKIPAMVVDRCGCS 109
DB 206 VHOANPRGSAGPCCPTPTKMSPINMLYFNGKEQIITGKIPAMVVDRCGCS 254
XX
XX RESULT 11
XX AAB20132
XX ID AAB20132 standard; Protein; 362 AA.
XX AC AAB20132;
XX DT 30-APR-2001 (first entry)
XX DB Turkey growth differentiation factor 8.
XX KW Turkey growth differentiation factor 8.
XX KW Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
XX KW vaccine; muscle; meat; cachexia; cardiant; turkey.

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OS Melegris gallopavo.
XX
PN WO200105820-A2.
XX
PD 25-JAN-2001.
XX
PF 20-JUL-2000; 2000WO-DK00413.
XX
PR 20-JUL-1999; 99DK-0001014.
PR 26-JUL-1999; 99US-0145275.
XX
PA (MEBI-) M & E BIOTECH AS.
XX
PI Halkier T, Mouritsen S, Klysner S;
XX
DR WPI; 2001-112680/12.
XX
PT Increasing the muscle mass of animals used in meat production by down
PT regulating growth differentiation factor 8 (GDF-8) activity in the
PT animal through induction of anti-GDF-8 antibody production -
XX
PS Example 1; Page 76-78; 110pp; English.
XX
CC The present sequence is that of turkey growth differentiation factor
CC 8 (GDF-8), also called myostatin. It is an object of the invention
CC to produce a recombinant therapeutic vaccine capable of effecting
CC down-regulation of GDF-8 in order to increase the muscle growth
CC rate of farm animals. Variants of GDF-8 (see AAB20145-53) are
CC provided that are capable of breaking autotolerance against
CC autologous GDF-8. These comprise a C-terminal portion of human
CC GDF-8 in which a portion of the native sequence is replaced by a
CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
CC P2 or P30. Nucleic acids encoding the GDF-8 variants can be used
CC for genetic immunisation of the animals. Down-regulation of GDF-8
CC activity is used to increase muscle mass by up to at least 45%
CC in cattle, pigs and poultry used for meat production, reducing the
CC need for antibiotic feed-additives. Anti-GDF8 vaccines can be used
CC to treat human diseases such as cancer cachexia where muscle atrophy
CC is pronounced and for patients suffering from acute and chronic
CC heart failure.
XX
SQ Sequence 362 AA;
Query Match 100.0%; Score 629; DB 22; Length 362;
Best Local Similarity 100.0%; Pred. No. 1e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 254 DFGLDCEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFVFLQKYPHTL 313
QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIYIGKIPAMVVDRCGS 109
DB 314 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIYIGKIPAMVVDRCGS 362
RESULT 12
AAU75623
ID AAU75623 standard; Protein; 374 AA.
XX
AC AAU75623;
XX
DT 21-MAY-2002 (first entry)
XX
DE Chicken promyostatin.
XX
KM Chicken; promyostatin; immunomodulator; antidepressant; anorectic;
KM neuroprotective; antidiabetic; growth differentiation factor receptor;
KM myostatin receptor; GDF; muscle tissue; adipose tissue; cachexia;
KM wasting disorder; anorexia; muscular dystrophy; neuromuscular disease;
KM metabolic disorder; obesity; type II diabetes.
XX
OS Gallus gallus.

XX
PN WO200210214-A2.
XX
PD 07-FEB-2002.
XX
PF 26-JUL-2001; 2001WO-US23615.
XX
PR 27-JUL-2000; 2000US-0626896.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Lee S, McPherron AC;
XX
DR WPI; 2002-217116/27.
DR N-PSDB; ABK15396.
XX
PT New growth differentiation factor (GDF) receptors and modulators,
PT useful for ameliorating wasting disorders such as cachexia, muscular
PT dystrophy or neuromuscular disease or a metabolic disorder such as
PT obesity or type II diabetes -
XX
PS Claim 22; Fig 1; 184pp; English.
XX
CC The invention relates to a substantially purified growth differentiation
CC factor (GDF) receptor, specifically a myostatin receptor, or its
CC functional peptide portion. Also described is a method of modulating an
CC effect of myostatin on a cell by contacting the cell with an agent that
CC affects myostatin signal transduction in the cell. The method and the
CC receptor are useful for ameliorating the severity of a pathological
CC condition characterised by an abnormal amount, development or metabolic
CC activity of muscle or adipose tissue in a subject, particularly a wasting
CC disorder (e.g. cachexia, anorexia, muscular dystrophy or neuromuscular
CC disease) or a metabolic disorder (e.g. obesity or type II diabetes). The
CC present sequence represents the amino acid sequence of chicken
CC promyostatin.
XX
SQ Sequence 374 AA;
Query Match 100.0%; Score 629; DB 23; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 266 DFGLDCEHSTESRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFVFLQKYPHTL 325
QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIYIGKIPAMVVDRCGS 109
DB 326 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIYIGKIPAMVVDRCGS 374
RESULT 13
AAR63160
ID AAR63160 standard; Protein; 375 AA.
XX
AC AAR63160;
XX
DT 23-JUN-1995 (first entry)
XX
DE Human growth differentiation factor-8 protein.
XX
KM Growth differentiation factor-8; GDF-8; cell proliferation;
KM adipocyte; obesity; transforming growth factor-beta.
XX
OS Homo sapiens.
XX
PN WO9421681-A.
XX
PD 29-SEP-1994.
XX
PF 18-MAR-1994; 94WO-US03019.
XX
PR 19-MAR-1993; 93US-0033923.

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XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.
PA
XX
PI Lee S, Mcpherron AC;
XX
DR WPI; 1994-316943/39.
DR Q-PSDB; Q76372.
XX
PT New growth differentiation factor 8 - useful for treatment and
PT diagnosis of cell proliferative disorders esp. of muscle.
XX
PS Claim 3; Page 58; 84pp; English.
XX
CC GDF-8 can be used to maintain cells before transplantation; to
CC improve efficiency of cell fusion and to treat obesity or diseases
CC related to abnormal adipocyte proliferation.
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 629; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
Db 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
Db 327 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375

RESULT 14
AAW69888
ID AAW69888 standard; Protein; 375 AA.
XX
AC AAW69888;
XX
DT 07-DEC-1998 (first entry)
XX
DE Chicken growth differentiation factor-8.
XX
KM Growth differentiation factor-8; GDF-8; chicken; transgenic animal;
KM transforming growth factor-beta; muscle; meat; inhibitor; obesity;
KM neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
KM therapy.
XX
OS Gallus sp.
XX
FH Key Location/Qualifiers
FT Cleavage-site 263..266
FT Protein 267..375
FT /label= Mat_protein
XX
PN WO9833887-A1.
XX
PD 06-AUG-1998.
XX
PF 05-FEB-1998; 98WO-US02479.
XX
PR 23-MAY-1997; 97US-0862445.
PR 05-FEB-1997; 97US-0795071.
PR 28-APR-1997; 97US-0847910.
XX
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Lee S, McPherron AC;
XX
DR WPI, 1998-437444/37.
DR N-PSDB; AAV45819.
XX
PT Transgenic animals with gene for growth differentiation factor-8
PT disrupted - have increased muscle and reduced cholesterol contents,
```

```
PT also use of GDF-8 inhibitors for treating cancer, obesity,
PT neuromuscular disease
XX
XX Example 9; Fig 14c; 125pp; English.
XX
CC This is the amino acid sequence of chicken growth differentiation
CC factor-8 (GDF-8), a novel member of the transforming growth factor-
CC beta superfamily that appears to relate to various cell
CC proliferative disorders, especially those involving muscle, nerve
CC and adipose tissue. The sequence was deduced from a cDNA clone
CC (see AAV45819) isolated from a skeletal muscle cDNA library. The
CC invention provides novel mammalian and avian GDF-8 proteins (see
CC AAW69883-92). A transgenic non-human animal is claimed in which
CC GDF-8 expression is disrupted or interfered with. Also claimed
CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
CC from these animals; (2) method for increasing muscle mass in
CC animals by administering an antibody (Ab) that binds to GDF-8; (3)
CC inhibiting the action of GDF-8 by treating foetal or adult muscle
CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
CC acid encoding a GDF-8 protein truncated by loss of the C-terminal
CC active fragment. The transgenic animals have increased muscle mass
CC and for poultry reduced cholesterol contents. Method (3) is used
CC to treat muscle wasting or neuromuscular diseases, muscular atrophy
CC and aging, particularly muscular dystrophy, spinal cord or
CC traumatic injuries, congestive or obstructive lung disease, AIDS
CC and cachexia. Method (4) is used to treat cancer of muscle,
CC connective tissue and bone, or obesity. Also (not claimed) GDF-8
CC can be used to maintain myoblasts intended for transplanting or to
CC improve efficiency of fusion. Ab can be used to detect and
CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
CC also for immunotherapy and in vivo imaging.
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 629; DB 19; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
Db 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
Db 327 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375

RESULT 15
AAW69891
ID AAW69891 standard; Protein; 375 AA.
XX
AC AAW69891;
XX
DT 07-DEC-1998 (first entry)
XX
DE Pig growth differentiation factor-8.
XX
KM Growth differentiation factor-8; GDF-8; pig; transgenic animal;
KM transforming growth factor-beta; muscle; meat; inhibitor; obesity;
KM neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
KM therapy.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT Cleavage-site 263..266
FT Protein 267..375
FT /label= Mat_protein
XX
PN WO9833887-A1.
XX
PD 06-AUG-1998.
```

PF 05-FEB-1998; 98WO-US02479.
XX
PR 23-MAY-1997; 97US-0862445.
PR 05-FEB-1997; 97US-0795071.
PR 28-APR-1997; 97US-0847910.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Lee S, McPherron AC;
XX
DR WPI; 1998-437444/37.
DR N-PSDB; AAV45822.
XX
PT Transgenic animals with gene for growth differentiation factor-8
PT disrupted - have increased muscle and reduced cholesterol contents,
PT also use of GDF-8 inhibitors for treating cancer, obesity,
PT neuromuscular disease
XX
PS Example 9, Fig 14f, 125pp; English.
XX
CC This is the amino acid sequence of porcine growth differentiation
CC factor-8 (GDF-8), a novel member of the transforming growth factor-
CC beta superfamily that appears to relate to various cell
CC proliferative disorders, especially those involving muscle, nerve
CC and adipose tissue. The sequence was deduced from a cDNA clone
CC (see AAV45822) isolated from a skeletal muscle cDNA library. The
CC invention provides novel mammalian and avian GDF-8 proteins (see
CC AAV69883-92). A transgenic non-human animal is claimed in which
CC GDF-8 expression is disrupted or interfered with. Also claimed
CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
CC from these animals; (2) method for increasing muscle mass in
CC animals by administering an antibody (Ab) that binds to GDF-8; (3)
CC inhibiting the action of GDF-8 by treating foetal or adult muscle
CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
CC acid encoding a GDF-8 protein truncated by loss of the C-terminal
CC active fragment. The transgenic animals have increased muscle mass
CC and for poultry reduced cholesterol contents. Method (3) is used
CC to treat muscle wasting or neuromuscular diseases, muscular atrophy
CC and aging, particularly muscular dystrophy, spinal cord or
CC traumatic injuries, congestive or obstructive lung disease, AIDS
CC and cachexia. Method (4) is used to treat cancer of muscle,
CC connective tissue and bone, or obesity. Also (not claimed) GDF-8
CC can be used to maintain myoblasts intended for transplanting or to
CC improve efficiency of fusion. Ab can be used to detect and
CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
CC also for immunotherapy and in vivo imaging.
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 629; DB 19; Length 375;
Best Local Similarity 100.0%; Pred. No. 1,1e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB DFGLDCEHSTESRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 109
DB VHOANPRGSAGPCCTPTKMSPINMLYFNGKEQIYGIKIPAMVVDRCGCS 375

Search completed: January 31, 2003, 18:20:10
Job time : 33 secs

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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:20:18 ; Search time 8 Seconds
(without alignments)
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Title: US-09-620-586B-11

Perfect score: 629
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Scoring table: BLOSUM62

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Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	629	100.0	126	9	US-09-859-211-6 Sequence 6, Appli
2	629	100.0	130	9	US-09-859-211-33 Sequence 33, Appl
3	629	100.0	226	9	US-09-859-211-35 Sequence 35, Appl
4	629	100.0	374	9	US-09-841-730-8 Sequence 8, Appli
5	629	100.0	375	9	US-09-841-730-2 Sequence 2, Appli
6	629	100.0	375	9	US-09-841-730-14 Sequence 14, Appl
7	629	100.0	375	9	US-09-841-730-18 Sequence 18, Appl
8	629	100.0	375	9	US-09-859-211-14 Sequence 23, Appl
9	629	100.0	375	9	US-09-859-211-23 Sequence 27, Appl
10	629	100.0	375	9	US-09-859-211-27 Sequence 29, Appl
11	629	100.0	375	9	US-09-859-211-29 Sequence 25, Appl
12	629	100.0	375	10	US-09-454-540-5 Sequence 4, Appli
13	629	100.0	376	9	US-09-841-730-4 Sequence 6, Appli
14	629	100.0	376	9	US-09-841-730-6 Sequence 12, Appl
15	629	100.0	376	9	US-09-859-211-12 Sequence 25, Appl
16	629	100.0	376	9	US-09-859-211-25 Sequence 38, Appl
17	629	100.0	376	9	US-09-813-398-38 Sequence 11, Appl
18	629	100.0	376	10	US-09-859-894A-11 Sequence 5, Appli
19	624	99.2	375	10	US-09-859-894A-5

20	623	99.0	375	9	US-09-841-730-10 Sequence 10, Appl
21	623	99.0	375	9	US-09-859-211-19 Sequence 19, Appl
22	622	98.9	109	10	US-09-754-826-2 Sequence 2, Appli
23	619	98.4	375	9	US-09-841-730-16 Sequence 16, Appl
24	619	98.4	375	9	US-09-859-211-31 Sequence 31, Appl
25	618	98.3	375	9	US-09-841-730-12 Sequence 12, Appl
26	618	98.3	375	9	US-09-859-211-21 Sequence 21, Appl
27	590	93.8	108	9	US-09-859-211-8 Sequence 8, Appli
28	581	92.4	126	10	US-09-454-540-4 Sequence 4, Appli
29	581	92.4	126	10	US-09-859-894A-4 Sequence 4, Appli
30	581	92.4	407	9	US-09-841-730-25 Sequence 25, Appl
31	581	92.4	407	10	US-09-454-540-2 Sequence 2, Appli
32	581	92.4	407	10	US-09-454-540-6 Sequence 6, Appli
33	581	92.4	407	10	US-09-859-894A-2 Sequence 2, Appli
34	581	92.4	408	9	US-09-813-398-33 Sequence 33, Appl
35	570	90.6	374	9	US-09-841-730-20 Sequence 20, Appl
36	564	89.7	136	9	US-09-841-730-29 Sequence 29, Appl
37	564	89.7	157	9	US-09-841-730-27 Sequence 27, Appl
38	512.5	81.5	128	10	US-09-205-658-317 Sequence 317, App
39	242	38.5	120	10	US-09-813-459-20 Sequence 20, Appl
40	242	38.5	120	12	US-10-115-406-20 Sequence 20, Appl
41	242	38.5	121	9	US-09-859-211-46 Sequence 46, Appl
42	242	38.5	121	9	US-09-880-708-24 Sequence 24, Appl
43	242	38.5	408	9	US-09-813-398-20 Sequence 20, Appl
44	242	38.5	408	9	US-09-813-398-22 Sequence 22, Appl
45	232.5	37.0	118	12	US-10-115-406-9 Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-859-211-6
Sequence 6, Application US/09859211
Patent No. US20020157125A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859,211
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 126
TYPE: PRT
ORGANISM: Mus musculus
US-09-859-211-6

Query Match 100.0%; Score 629; DB 9; Length 126;
Best local Similarity 100.0%; Pred. No. 1.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYSGEGCEVFVLOKYPHTL 60
Db 18 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYSGEGCEVFVLOKYPHTL 77
QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNKGQIITYGKIPAMVVDRCGCS 109

Db 78 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 126

RESULT 2
US-09-859-211-33

/ Sequence 33, Application US/09859211
/ Patent No. US20020157125A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Se-Jin
/ APPLICANT: McPherron, Alexandra C.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
/ FILE REFERENCE: 07265/144001
/ CURRENT APPLICATION NUMBER: US/09/859,211
/ CURRENT FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 09/019,070
/ PRIOR FILING DATE: 1998-02-05
/ PRIOR APPLICATION NUMBER: 08/862,445
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 08/847,910
/ PRIOR FILING DATE: 1997-04-28
/ PRIOR APPLICATION NUMBER: 08/795,071
/ PRIOR FILING DATE: 1997-02-05
/ PRIOR APPLICATION NUMBER: 08/525,596
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: PCT/US94/03019
/ PRIOR FILING DATE: 1994-03-18
/ PRIOR APPLICATION NUMBER: 08/033,923
/ PRIOR FILING DATE: 1993-03-19
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-09-859-211-33

Query Match 100.0%; Score 629; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 2e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTHL 60
Db 22 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTHL 81

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 109
Db 82 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 130

RESULT 3

US-09-859-211-35
/ Sequence 35, Application US/09859211
/ Patent No. US20020157125A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Se-Jin
/ APPLICANT: McPherron, Alexandra C.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
/ FILE REFERENCE: 07265/144001
/ CURRENT APPLICATION NUMBER: US/09/859,211
/ CURRENT FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 09/019,070
/ PRIOR FILING DATE: 1998-02-05
/ PRIOR APPLICATION NUMBER: 08/862,445
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 08/847,910
/ PRIOR FILING DATE: 1997-04-28
/ PRIOR APPLICATION NUMBER: 08/795,071
/ PRIOR FILING DATE: 1997-02-05
/ PRIOR APPLICATION NUMBER: 08/525,596
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: PCT/US94/03019
/ PRIOR FILING DATE: 1994-03-18

/ PRIOR APPLICATION NUMBER: 08/033,923
/ PRIOR FILING DATE: 1993-03-19
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 226
/ TYPE: PRT
/ ORGANISM: Gallus gallus
US-09-859-211-35

Query Match 100.0%; Score 629; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.5e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTHL 60
Db 118 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTHL 177

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 109
Db 178 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 226

RESULT 4
US-09-841-730-8

/ Sequence 8, Application US/09841730
/ Patent No. US20020157126A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Se-Jin
/ APPLICANT: McPherron, Alexandra C.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
/ TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
/ FILE REFERENCE: JH1470-2
/ CURRENT APPLICATION NUMBER: US/09/841,730
/ CURRENT FILING DATE: 2001-04-24
/ PRIOR APPLICATION NUMBER: 09/626,896
/ PRIOR FILING DATE: 2000-07-27
/ PRIOR APPLICATION NUMBER: 09/485,046
/ PRIOR FILING DATE: 2000-01-31
/ PRIOR APPLICATION NUMBER: PCT/US98/15598
/ PRIOR FILING DATE: 1998-07-28
/ PRIOR APPLICATION NUMBER: 60/054,461
/ PRIOR FILING DATE: 1997-08-01
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 374
/ TYPE: PRT
/ ORGANISM: Gallus gallus
US-09-841-730-8

Query Match 100.0%; Score 629; DB 9; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTHL 60
Db 266 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTHL 325

QY 61 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 109
Db 326 VHQANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 374

RESULT 5
US-09-841-730-2

/ Sequence 2, Application US/09841730
/ Patent No. US20020157126A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Se-Jin
/ APPLICANT: McPherron, Alexandra C.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
/ TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME


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; FILE REFERENCE: JHUI470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-841-730-2
```

```
Query Match 100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCEFEVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 375
```

```
RESULT 6
US-09-841-730-14
; Sequence 14, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; FILE REFERENCE: JHUI470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Porcine
US-09-841-730-14
```

```
Query Match 100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCEFEVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 375
```

```
RESULT 7
US-09-841-730-18
; Sequence 18, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; FILE REFERENCE: JHUI470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-09-841-730-18
```

```
Query Match 100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCEFEVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 375
```

```
RESULT 8
US-09-859-211-14
; Sequence 14, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-211-14
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```
Query Match      100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 60
   |||||
Db 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109
   |||||
Db 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 375

RESULT 9
US-09-859-211-23
; Sequence 23, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-859-211-23

Query Match      100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 60
   |||||
Db 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109
   |||||
Db 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 375

RESULT 10
US-09-859-211-27
; Sequence 27, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
```

```
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-09-859-211-27

Query Match      100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 60
   |||||
Db 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109
   |||||
Db 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 375

RESULT 11
US-09-859-211-29
; Sequence 29, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Porcine
US-09-859-211-29

Query Match      100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 60
   |||||
Db 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVFLQKYPHTL 326
```

QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 375

RESULT 12
US-09-454-540-5

; Sequence 5, Application US/09454540
; Patent No. US20010053358A1
; GENERAL INFORMATION:
; APPLICANT: Se-Jin Lee and Alexandra McPherron
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/454,540
; FILING DATE: 06-DEC-1999
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/795,671
; FILING DATE: February 6, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, PH.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/106001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: GDF-8
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..375
US-09-454-540-5

Query Match 100.0%; Score 629; DB 10; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVLOKYPHTHL 60
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVLOKYPHTHL 326

QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 375

RESULT 13
US-09-841-730-4
; Sequence 4, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:

; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; PRIORITY FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-841-730-4

Query Match 100.0%; Score 629; DB 9; Length 376;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVLOKYPHTHL 60
DB 268 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVLOKYPHTHL 327

QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109
DB 328 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 376

RESULT 14

US-09-841-730-6
; Sequence 6, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; PRIORITY FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-841-730-6

Query Match 100.0%; Score 629; DB 9; Length 376;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVLOKYPHTHL 60
DB 268 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVLOKYPHTHL 327

QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109

Db 328 VHQANPRGSAGPCCPTKMSPINMLYFNGKEQILYGIKIPAMVVDRCGCS 376

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RESULT 15
US-09-859-211-12
; Sequence 12, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0.0
; SEQ ID NO 12
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-859-211-12

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[illegible]

Search completed: January 31, 2003, 18:27:18
Job time : 9 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: January 31, 2003, 18:17:50 ; Search time 11.5 Seconds
(without alignments)
278.878 Million cell updates/sec

Title: US-09-620-586B-11

Perfect score: 629

Sequence: 1 DFGLDGDEHSTESRCRYPL.....KEQIYGRIPAMVVDRCGCS 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	629	100.0	126	2	US-08-525-596B-6
2	629	100.0	126	3	US-09-177-860A-6
3	629	100.0	126	4	US-09-378-238-6
4	629	100.0	126	4	US-09-451-501-6
5	629	100.0	130	4	US-09-378-238-21
6	629	100.0	225	4	US-09-378-238-19
7	629	100.0	375	2	US-08-525-596B-14
8	629	100.0	375	2	US-08-765-875-5
9	629	100.0	375	3	US-08-795-671-5
10	629	100.0	375	3	US-09-177-860A-14
11	629	100.0	375	4	US-09-252-149B-29
12	629	100.0	375	4	US-09-252-149B-32
13	629	100.0	375	4	US-09-252-149B-34
14	629	100.0	375	4	US-09-252-149B-35
15	629	100.0	375	4	US-09-378-238-14
16	629	100.0	375	4	US-09-451-501-14
17	629	100.0	375	4	US-09-451-501-19
18	629	100.0	375	4	US-09-451-501-21
19	629	100.0	375	4	US-09-451-501-23
20	629	100.0	375	4	US-09-451-501-27
21	629	100.0	376	2	US-08-525-596B-12
22	629	100.0	376	3	US-09-177-860A-12
23	629	100.0	376	3	US-08-891-789B-6
24	629	100.0	376	4	US-09-252-149B-27
25	629	100.0	376	4	US-09-252-149B-28
26	629	100.0	376	4	US-09-378-238-12
27	629	100.0	376	4	US-09-451-501-12

28	629	100.0	376	4	US-09-451-501-25	Sequence 25, Appl
29	623	99.0	375	4	US-09-252-149B-30	Sequence 30, Appl
30	619	98.4	375	4	US-09-252-149B-33	Sequence 33, Appl
31	618	98.3	375	3	US-08-891-789B-2	Sequence 2, Appl
32	618	98.3	375	4	US-09-252-149B-2	Sequence 2, Appl
33	618	98.3	375	4	US-09-252-149B-31	Sequence 31, Appl
34	590	93.8	108	2	US-08-525-596B-8	Sequence 8, Appl
35	590	93.8	108	3	US-09-177-860A-8	Sequence 8, Appl
36	590	93.8	108	4	US-09-378-238-8	Sequence 8, Appl
37	590	93.8	108	4	US-09-451-501-8	Sequence 8, Appl
38	581	92.4	126	1	US-08-247-907A-2	Sequence 2, Appl
39	581	92.4	126	1	US-08-452-772-2	Sequence 2, Appl
40	581	92.4	126	2	US-08-765-875-4	Sequence 4, Appl
41	581	92.4	126	3	US-08-795-671-4	Sequence 4, Appl
42	581	92.4	126	4	US-09-414-234-2	Sequence 2, Appl
43	581	92.4	126	4	US-08-919-850-2	Sequence 2, Appl
44	581	92.4	126	5	PCT-US94-05288-2	Sequence 2, Appl
45	581	92.4	362	1	US-08-247-907A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-525-596B-6
; Sequence 6, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huyuh, Thanh
; APPLICANT: Lee, Se-jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-525-596B-6

Query Match 100.0%; Score 629; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.7e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDGDEHSTESRCRYPLTVDFEAFGWDWITADPKRYKANYCSGCEGFVFLQKYPHTL 60
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Db 18 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFVFLQKYPHTL 77

Qy 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109
Db 78 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 126

RESULT 2

US-09-177-860A-6
; Sequence 6, Application US/09177860A
; Patent No. 6096506
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/177, 860A
; FILING DATE: 23-OCT-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/525,596
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D, Lisa A.
; REGISTRATION NUMBER: 38, 347
; REFERENCE/DOCKET NUMBER: 07265/075003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-677-1456
; TELEFAX: 858-677-1465
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-177-860A-6

Query Match 100.0%; Score 629; DB 3; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.7e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFVFLQKYPHTL 60
Db 18 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFVFLQKYPHTL 77

Qy 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109
Db 78 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 126

RESULT 3

US-09-378-238-6
; Sequence 6, Application US/09378238
; Patent No. 6465239
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
; TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

; TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
; FILE REFERENCE: JHU1120-9

; CURRENT APPLICATION NUMBER: US/09/378,238
; CURRENT FILING DATE: 1999-08-19
; EARLIER APPLICATION NUMBER: 08/795,071
; EARLIER FILING DATE: 1997-02-05
; EARLIER APPLICATION NUMBER: 08/525,596
; EARLIER FILING DATE: 1995-10-25
; EARLIER APPLICATION NUMBER: PCT/US94/03019
; EARLIER FILING DATE: 1994-03-18
; EARLIER APPLICATION NUMBER: 08/033,923
; EARLIER FILING DATE: 1993-03-19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-378-238-6

Query Match 100.0%; Score 629; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.7e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 18 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIAPKRYKANYCSGCECFVFLQKYPHTL 77

Qy 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 109
Db 78 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIYKIPAMVVDRCGCS 126

RESULT 4

US-09-451-501-6
; Sequence 6, Application US/09451501
; Patent No. 6468535
; GENERAL INFORMATION:
; APPLICANT: Se-Jin Lee et al.,
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,501
; FILING DATE: 30-No. 6468535-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,071
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/US94/03019
; FILING DATE: 18-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Haile, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/105001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 6
US-09-451-501-6

Query Match 100.0%; Score 629; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.7e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 18 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECFVFLQKYPHTL 77

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYENGKEQIYGIKIPAMVVDRCGCS 109
DB 78 VHOANPRGSAGPCCPTPTKMSPINMLYENGKEQIYGIKIPAMVVDRCGCS 126

RESULT 5

US-09-378-238-21
Sequence 21, Application US/09378238
Patent No. 6465239
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
FILE REFERENCE: JH01120-9
CURRENT APPLICATION NUMBER: US/09/378,238
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1997-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1994-03-18
EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 130
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-378-238-21

Query Match 100.0%; Score 629; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.8e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 22 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECFVFLQKYPHTL 81

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYENGKEQIYGIKIPAMVVDRCGCS 109
DB 82 VHOANPRGSAGPCCPTPTKMSPINMLYENGKEQIYGIKIPAMVVDRCGCS 130

RESULT 6

US-09-378-238-19
Sequence 19, Application US/09378238
Patent No. 6465239
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
FILE REFERENCE: JH01120-9
CURRENT APPLICATION NUMBER: US/09/378,238

CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1997-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1994-03-18
EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 225
TYPE: PRT
ORGANISM: Gallus gallus
US-09-378-238-19

Query Match 100.0%; Score 629; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 7.3e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 117 DFGLDCEHSTESRCRCRYPLTVDFEAFGWDWIIAPKRYKANYCSGCECFVFLQKYPHTL 176

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYENGKEQIYGIKIPAMVVDRCGCS 109
DB 177 VHOANPRGSAGPCCPTPTKMSPINMLYENGKEQIYGIKIPAMVVDRCGCS 225

RESULT 7

US-08-525-596B-14
Sequence 14, Application US/08525596B
Patent No. 5827733
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
FILING DATE: 19-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07265/075001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-525-596B-14

Query Match 100.0%; Score 629; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 60
DB 267 DFGDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 375

RESULT 8

US-08-765-875-5
; Sequence 5, Application US/08765875
; Patent No. 5914234
; GENERAL INFORMATION:
; APPLICANT: LEE, SE-JIN
; APPLICANT: MCPHERRON, ALEXANDRA C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,875
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,958
; FILING DATE:
; APPLICATION NUMBER: US/08/272,763
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN PH.D., LISA A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: PD3641
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619/455-5110
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: GDF-8
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..375
; US-08-765-875-5

Query Match 100.0%; Score 629; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 60
DB 267 DFGDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 375

RESULT 9

US-08-795-671-5
; Sequence 5, Application US/08795671
; Patent No. 6008434
; GENERAL INFORMATION:
; APPLICANT: Se-jin Lee and Alexandra McPherron
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,671
; FILING DATE: February 6, 1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: HALL, PH.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/106001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: GDF-8
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..375
; US-08-795-671-5

Query Match 100.0%; Score 629; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 60
DB 267 DFGDDEHSTESRCRYPPLTVDFEAFGWDWIIAPKRYKANYCSGCEFFVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 375

RESULT 10

US-09-177-860A-14
; Sequence 14, Application US/09177860A
; Patent No. 6096506
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-jin
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halile, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPES: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-177-860A-14

Query Match 100.0%; Score 629; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 375

RESULT 11
US-09-252-149B-29
Sequence 29, Application US/09252149B
Patent No. 6369201
GENERAL INFORMATION:
APPLICANT: Barker, Christopher A.
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
FILE REFERENCE: 9001-0042
CURRENT APPLICATION NUMBER: US/09/252,149B
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/075,213
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-252-149B-29

Query Match 100.0%; Score 629; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 375

RESULT 12
US-09-252-149B-32
Sequence 32, Application US/09252149B
Patent No. 6369201
GENERAL INFORMATION:
APPLICANT: Barker, Christopher A.
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
FILE REFERENCE: 9001-0042
CURRENT APPLICATION NUMBER: US/09/252,149B
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/075,213
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 375
TYPE: PRT
ORGANISM: Sus scrofa
US-09-252-149B-32

Query Match 100.0%; Score 629; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 326
QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCTPTKMSPINMLYFNKGKQIYGIKIPAMVVDRCGCS 375

RESULT 13
US-09-252-149B-34
Sequence 34, Application US/09252149B
Patent No. 6369201
GENERAL INFORMATION:
APPLICANT: Barker, Christopher A.
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
FILE REFERENCE: 9001-0042
CURRENT APPLICATION NUMBER: US/09/252,149B
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/075,213
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 375
TYPE: PRT
ORGANISM: Gallus gallus
US-09-252-149B-34

Query Match 100.0%; Score 629; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFEVFLQKYPHTL 326

OY 61 VHQANPRGSAGPCCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375

RESULT 14

US-09-252-149B-35
; Sequence 35, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Melagris gallopavo
US-09-252-149B-35

Query Match 100.0%; Score 629; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGLDCEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326
OY 61 VHQANPRGSAGPCCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375

RESULT 15

US-09-378-238-14
; Sequence 14, Application US/09378238
; Patent No. 6465239
; GENERAL INFORMATION:
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
; TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
; TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
; FILE REFERENCE: JHU1120-9
; CURRENT APPLICATION NUMBER: US/09/378,238
; CURRENT FILING DATE: 1999-08-19
; EARLIER APPLICATION NUMBER: 08/795,071
; EARLIER FILING DATE: 1997-02-05
; EARLIER APPLICATION NUMBER: 08/525,596
; EARLIER FILING DATE: 1995-10-25
; EARLIER APPLICATION NUMBER: PCT/US94/03019
; EARLIER FILING DATE: 1994-03-18
; EARLIER APPLICATION NUMBER: 08/033,923
; EARLIER FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-378-238-14

Query Match 100.0%; Score 629; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGLDCEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326
OY 61 VHQANPRGSAGPCCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375

Search completed: January 31, 2003, 18:18:23
Job time: 12.5 secs